

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1          5          10          15
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
          20          25          30
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
          35          40          45
Thr Leu Ser Arg Trp Met
          50

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1          5          10          15
Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
          20          25          30
Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
          35          40          45
Thr Ser Leu Pro
          50

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
 1 5 10 15

Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
 1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
 20 25 30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
 35 40 45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
 50 55 60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp
 65 70

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
20

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Thr Cys Gly Arg Gln Trp
1 5

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
50 55 60

Ser Leu Gly Ser Cys Gly
65 70

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Ser	Val	Thr	Ala	Cys	Phe	Trp	Ile	Cys	Arg
1				5					10

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Thr	Ala	Ser	Arg	Arg	Cys	Ala	Pro	Thr	Ser	Thr	Arg	Ser	Ser	Cys	Cys
1				5					10					15	

Arg	Arg	Thr	Gly	Phe	Thr	His	Val	Cys	Cys	Ser	Ser	His	Phe	Ile	Ser
			20					25					30		

Lys	Phe	Gly	Arg	Thr	Pro	His	Phe	Ser	Cys	Ala	Ser	Ser	Leu	Thr	Arg
		35					40					45			

Pro	Pro	Ser	Ala	Thr	Pro	Ser
		50				55

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Lys	Pro	Arg	Thr	Gln	Gly	Cys	Arg	Trp	Gly	Pro	Arg	Ala	Pro	Pro	Ala
1				5					10					15	

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
 20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
 1 5 10 15

Pro Arg Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Val Gly Ser Ser Arg Gly Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
 1 5 10 15

Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
 20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
 35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Gly Leu Ser Glu Cys Pro Ala Lys Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg
 1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu
 20 25 30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1           5           10           15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
                20           25           30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
          35           40           45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50           55           60

Ala Val Gly Val Lys Tyr
65           70

```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys
1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1           5           10           15

```

```

Pro Ala Met  Pro Arg Ala  Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
      20                      25                      30

Arg Ser His  Tyr Arg Glu Val  Leu Pro Leu Ala Thr Phe Val Arg Arg
      35                      40                      45

Leu Gly Pro  Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
      50                      55                      60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
      65                      70                      75                      80

Xaa Xaa Pro  Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
      85                      90                      95

Xaa Leu Val  Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
      100                     105                     110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      115                     120                     125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      130                     135                     140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      145                     150                     155                     160

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
      165                     170                     175

Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
      180                     185                     190

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
      195                     200                     205

Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
      210                     215                     220

```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
1                      5                      10                      15

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
      20                      25                      30

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
      35                      40                      45

```

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
 50 55 60

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 65 70 75 80

Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 85 90 95

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
 100 105 110

Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
 115 120 125

Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
 130 135 140

Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
 145 150 155 160

Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
 165 170 175

Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
 180 185 190

His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
 195 200 205

Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
 210 215 220

Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser
 225 230 235 240

Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
 245 250 255

Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
 260 265 270

Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285

Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300

Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320

Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Gly 1	Asp	Pro	Gly 5	Gln	Val	Pro	Ala	Leu 10	Ala	Asp	Glu	Cys	Val	Arg	Arg
Arg	Ala	Ala	Gln 20	Val	Phe	Leu	Leu	Cys 25	His	Gly	Asp	His	Val 30	Ser	Lys
Glu	Gln	Ala 35	Leu	Phe	Leu	Pro	Glu 40	Glu	Cys	Leu	Glu	Gln 45	Val	Ala	Lys
His 50	Trp	Asn	Gln	Thr	Ala	Leu 55	Glu	Glu	Gly	Ala	Ala	Ala	Gly	Ala	Val
Gly 65	Ser	Arg	Gly	Gln	Ala 70	Ala	Ser	Gly	Ser	Gln 75	Ala	Arg	Pro	Ala	Asp 80
Val	Gln	Thr	Pro	Leu	His	Pro	Gln	Ala							

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Arg	Ala	Ala	Ala	Asp	Cys	Glu	His	Gly	Leu	Arg	Arg	Gly	Ser	Gln	Asn
1				5					10					15	
Val	Pro	Gln	Arg	Lys	Glu	Gly	Arg	Ala	Ser	His	Leu	Glu	Gly	Glu	Gly
			20					25					30		
Thr	Val	Gln	Arg	Ala	Gln	Leu	Arg	Ala	Gly	Ala	Ala	Pro	Arg	Pro	Pro
		35					40					45			
Gly	Arg	Leu	Cys	Ala	Gly	Pro	Gly	Arg	Tyr	Pro	Gln	Gly	Leu	Ala	His
	50					55					60				
Leu	Arg	Ala	Ala	Cys	Ala	Gly	Pro	Gly	Pro	Ala	Ala				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15

Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 30

His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45

Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60

Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80

Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60

Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
 1 5 10 15
 Asp Pro Gly Pro Arg Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
 1 5 10 15
 Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
 20 25 30
 Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
 35 40 45
 Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
 50 55 60
 Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
 65 70 75 80
 Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
 85 90 95
 Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
 100 105 110
 Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile
 115 120 125
 Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

His Gly Leu Pro Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp
1           5           10          15
Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg
                20          25          30
Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro
          35           40           45
Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala
      50           55           60
Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg
65           70           75           80
Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met
                85           90           95
Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser
          100          105          110
Arg Arg Ala Leu Arg Pro Arg Glu Gly Gly Ala Ala His Thr Gln Ala
          115          120          125
Arg Thr Ala Gly Ser Leu Arg Pro Glu
          130          135

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Val Phe Gly Arg Gly Leu His Val Arg Leu Lys Ala Glu Cys Pro Ala
1           5           10          15
Glu Ala

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Ala Ser Val Gln Pro Arg Ala Glu Cys Pro Ala His Leu Pro Ser Ser
1           5           10           15

Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro
          20           25           30

His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro
          35           40           45

Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro
          50           55           60

Pro Pro Ser Arg Trp Arg Pro
          65           70

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro
1           5           10           15

Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser
          20           25           30

Asn Trp Gly Glu Val Leu Trp Glu
          35           40

```

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys
 1 5 10 15
 Lys Lys

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro
 1 5 10 15
 Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys
 20 25 30
 Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala
 35 40 45
 Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu
 50 55 60
 Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa
 65 70 75 80
 Gly Xaa Pro Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg
 1 5 10 15
 Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly
 20 25 30

Arg

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
1 5 10 15

Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
20 25 30

Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
35 40 45

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
50 55 60

Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
65 70 75 80

Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
85 90 95

Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
100 105 110

Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
115 120 125

Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
130 135 140

Cys	His	Leu	Pro	Asp	Pro	Pro	Lys	Lys	Pro	Pro	Leu	Trp	Arg	Val	Arg
145					150					155					160

Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
165 170 175

Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
180 185 190

Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
195 200 205

Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
210 215 220

Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335
 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540

Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	
545					550					555					560	
Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	
				565					570						575	
Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	
			580					585						590		
Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	
		595					600					605				
Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
	610					615					620					
His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	
625					630					635					640	
Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Xaa	Asn	Ser	Pro	
				645					650						655	
Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
			660					665					670			
Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
		675					680					685				
Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
	690					695					700					
Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
705					710					715					720	
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
				725					730						735	
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
			740					745						750		
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
		755					760						765			
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
	770					775					780					
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
785					790					795					800	
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
				805					810					815		
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn	
			820					825					830			
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
		835					840					845				
Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	
	850					855					860					

Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
 1 5 10 15
 His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
 20 25 30
 Pro Ala Pro Leu Gly Val
 35

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
1 5 10 15

Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
20 25 30

Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
85 90

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Phe Gln Phe
 1

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Lys Lys Lys Lys Lys Lys Lys Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 56..3454
 (D) OTHER INFORMATION: /note= "refined sequence of hTRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC							106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His							
	5		10			15	

TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro	
20 25 30	
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala	
35 40 45	
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro	
50 55 60 65	
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val	
70 75 80	
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu	
85 90 95	
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu	
100 105 110	
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp	
115 120 125	
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC	490
Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly	
130 135 140 145	
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG	538
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu	
150 155 160	
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG	586
Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln	
165 170 175	
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC	634
Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro	
180 185 190	
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG	682
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu	
195 200 205	
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG	730
Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly	
210 215 220 225	
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC	778
Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly	
230 235 240	
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC	826
Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala	
245 250 255	

CAC His	CCG Pro	GGC Gly	AGG Arg	ACG Thr	CGT Arg	GGA Gly	CCG Pro	AGT Ser	GAC Asp	CGT Arg	GGT Gly	TTC Phe	TGT Cys	GTG Val	GTG Val	874
	260						265					270				
TCA Ser	CCT Pro	GCC Ala	AGA Arg	CCC Pro	GCC Ala	GAA Glu	GAA Glu	GCC Ala	ACC Thr	TCT Ser	TTG Leu	GAG Glu	GGT Gly	GCG Ala	CTC Leu	922
	275					280					285					
TCT Ser	GGC Gly	ACG Thr	CGC Arg	CAC His	TCC Ser	CAC His	CCA Pro	TCC Ser	GTG Val	GGC Gly	CGC Arg	CAG Gln	CAC His	CAC His	GCG Ala	970
	290				295					300					305	
GGC Gly	CCC Pro	CCA Pro	TCC Ser	ACA Thr	TCG Ser	CGG Arg	CCA Pro	CCA Pro	CGT Arg	CCC Pro	TGG Trp	GAC Asp	ACG Thr	CCT Pro	TGT Cys	1018
				310					315					320		
CCC Pro	CCG Pro	GTG Val	TAC Tyr	GCC Ala	GAG Glu	ACC Thr	AAG Lys	CAC His	TTC Phe	CTC Leu	TAC Tyr	TCC Ser	TCA Ser	GGC Gly	GAC Asp	1066
		325					330					335				
AAG Lys	GAG Glu	CAG Gln	CTG Leu	CGG Arg	CCC Pro	TCC Ser	TTC Phe	CTA Leu	CTC Leu	AGC Ser	TCT Ser	CTG Leu	AGG Arg	CCC Pro	AGC Ser	1114
	340						345					350				
CTG Leu	ACT Thr	GGC Gly	GCT Ala	CGG Arg	AGG Arg	CTC Leu	GTG Val	GAG Glu	ACC Thr	ATC Ile	TTT Phe	CTG Leu	GGT Gly	TCC Ser	AGG Arg	1162
	355					360					365					
CCC Pro	TGG Trp	ATG Met	CCA Pro	GGG Gly	ACT Thr	CCC Pro	CGC Arg	AGG Arg	TTG Leu	CCC Pro	CGC Arg	CTG Leu	CCC Pro	CAG Gln	CGC Arg	1210
	370				375				380					385		
TAC Tyr	TGG Trp	CAA Gln	ATG Met	CGG Arg	CCC Pro	CTG Leu	TTT Phe	CTG Leu	GAG Glu	CTG Leu	CTT Leu	GGG Gly	AAC Asn	CAC His	GCG Ala	1258
				390					395				400			
CAG Gln	TGC Cys	CCC Pro	TAC Tyr	GGG Gly	GTG Val	CTC Leu	CTC Leu	AAG Lys	ACG Thr	CAC His	TGC Cys	CCG Pro	CTG Leu	CGA Arg	GCT Ala	1306
		405					410					415				
GCG Ala	GTC Val	ACC Thr	CCA Pro	GCA Ala	GCC Ala	GGT Gly	GTC Val	TGT Cys	GCC Ala	CGG Arg	GAG Glu	AAG Lys	CCC Pro	CAG Gln	GGC Gly	1354
	420					425					430					
TCT Ser	GTG Val	GCG Ala	GCC Ala	CCC Pro	GAG Glu	GAG Glu	GAG Glu	GAC Asp	ACA Thr	GAC Asp	CCC Pro	CGT Arg	CGC Arg	CTG Leu	GTG Val	1402
	435				440						445					
CAG Gln	CTG Leu	CTC Leu	CGC Arg	CAG Gln	CAC His	AGC Ser	AGC Ser	CCC Pro	TGG Trp	CAG Gln	GTG Val	TAC Tyr	GGC Gly	TTC Phe	GTG Val	1450
	450				455			460							465	
CGG Arg	GCC Ala	TGC Cys	CTG Leu	CGC Arg	CGG Arg	CTG Leu	GTG Val	CCC Pro	CCA Pro	GGC Gly	CTC Leu	TGG Trp	GGC Gly	TCC Ser	AGG Arg	1498
				470				475				480				
CAC His	AAC Asn	GAA Glu	CGC Arg	CGC Arg	TTC Phe	CTC Leu	AGG Arg	AAC Asn	ACC Thr	AAG Lys	AAG Lys	TTC Phe	ATC Ile	TCC Ser	CTG Leu	1546
		485					490					495				

GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565 570 575	1786
CCG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266

ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys 370 375 380	2698
ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val 885 890 895	2746
GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala 900 905 910	2794
CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro 915 920 925	2842
TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp 930 935 940 945	2890
TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn 950 955 960	2938
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val 965 970 975	2986

TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser 980 985 990	3034
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala 995 1000 1005	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val 1010 1015 1020 1025	3130
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser 1030 1035 1040	3178
CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly 1045 1050 1055	3226
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu 1060 1065 1070	3274
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr 1075 1080 1085	3322
GTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg 1090 1095 1100 1105	3370
AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro 1110 1115 1120	3418
CCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCCACAG Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1125 1130	3471
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGGCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTTGCC	3591
CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCACG	3651
CCAAGGGCTG AGTGTCACGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCCAG GGCCAGCTTT TCYTCAACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTGCGC ATTGTTCAAC CYTCGCCCTG CCYTCCCTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGRAA	4011
AAAAAAAAA AAAAAAAAAA AAAAAA	4037

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1           5           10           15
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
          20           25           30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
          35           40           45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
          50           55           60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65           70           75           80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
          85           90           95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
          100          105          110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
          115          120          125
)
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
          130          135          140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
          145          150          155          160
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
          165          170          175
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
          180          185          190
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
          195          200          205
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
          210          215          220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
          225          230          235          240
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
          245          250          255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
          260          265          270

```

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Trp Xaa Gly Xaa Ser Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Trp Leu Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Thr
1 5 10 15

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Arg Lys Xaa Xaa
20 25 30

Trp

(xii) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 10..11
      (D) OTHER INFORMATION: /product= "OTHER"
                           /note= "Xaa = hydrophobic amino acid,
                           Ala, Leu, Ile, Val, Pro, Phe, Trp
                           or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 12
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = Gln or Arg"
```

[illegible][illegible][illegible]

```
(1X) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 28..29
      (D) OTHER INFORMATION: /product= "OTHER"
                           /note= "Xaa = Phe or Tyr"
```

```
(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 31
  (D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = Lys or His"
```

```
(*) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1          5          10          15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20          25          30

Xaa Trp
```

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29..30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1          5          10          15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
          20          25          30
Xaa Xaa Trp
          35

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1          5          10          15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
          20          25          30
Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
          35          40

```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr
1				5					10							15
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa
			20					25							30	
Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile					
			35					40								

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Glu	Xaa	Xaa	Val	Xaa
1			5	

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Pro	Lys	Xaa	Xaa	Xaa
1			5				10			

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Xaa	Arg	Xaa	Ile	Xaa
1			5	

(ii) MOLECULE TYPE: peptide

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
1 5 10 15
Xaa

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Phe Phe Tyr Xaa Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Phe Phe Tyr Val Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

AGNTTYATHC CNAARCC

17

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

TANGTRTCRT ANGC

14

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGNATHCCNC ARGG

14

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

SWNCCYTGN G DATNCC

17

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Leu Val Asp Asp Phe Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

YTNGTNGAYG AYTYYT

17

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Asp Asp Phe Leu Leu Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GTNACNARNA RRAARTCRTC

20

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GTGAAGGCAC TGTTACGCG

19

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.15 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGCGTG GGTG AGGTGAGGTG

20

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.14 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

CTGTGCTGGG CCTGGACGAT A

21

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

AGCTTGTTCT CCATGTCGCC GTAG

24

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.9 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TGACCCCAGG AGTGGCAGG

19

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.10 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "TCP1.11 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.12 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.13 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.16 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

TTTCCGTGTT GAGTGTTTC

19

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCPl.17 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GTCACCGTGT TGGGCAGG

18

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.19 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GCTACCTGCC CAACACGG

18

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.20 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GCGCGAAGAA CGTGCTGG

18

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.21 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

CACTGCTCCT TGTCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.22 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

TTCCCAAGGA CTTTGTTC

19

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.24 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

TGTTCTCAA GACGCACTG

19

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.25 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TACTGCGTGC GTCGGTATG

19

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.26 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGTCTTGCGG CTGAAGTGT

19

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.27 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TGGTTCACCT GCTGGCAG

19

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.28 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GTGGTTTCTG TGTGGTGTC

19

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.29 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GACACCACAC AGAAACCAC

19

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.30 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GTGCCAGCAG GTGAACCAG

19

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.32B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCAGTGCCTC TTGAGGAGC

19

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.33 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGGAACCATA GCGTCAGGGA G

21

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.34 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCCTCCCTG ACGCTATGGT T

21

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GCKCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35t primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GCTCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.36 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

ACGCCGAGAC CAAGCACTTC

20

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.38 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CCAAAGAGGT GGCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.39 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

AAGGCCAGCA CGTTCTTCGC

20

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.40 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

CACGTTCTGTG CGGCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.41 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CCTTCACCAC CAGCGTGCG

19

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.42 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GGCGACGACG TGCTGGTTC

19

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.43 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGCTCAGGGG CAGCGCCAC

19

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.44 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

CTGGCAGGTG TACGGCTTC

19

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.45 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GCGTGGACCG AGTGACCGTG GTTTC

25

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.46 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GACGTGGTGG CCGCGATGTG G

21

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.47 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAAGTCTGCC GTTCCCAAG AG

22

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.48 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GACACCACAC AGAAACCACG GTCAC

25

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCPl.49 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

CGCCCCCTCC TTCCGCCAGG T

21

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.50 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

CGAAGCCGAA GGCCAGCACG TTCTT

25

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCPl.51 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GGTGGCCCGA GTGCTGCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.52 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GTAGCTGCGC ACGCTGGTGG TGAAG

25

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.53 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

TGGGCGACGA CGTGCTGGTT CA

22

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.54 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

TATGGTTCCA GGCCCGTTCG CATCC

25

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.55 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CCAGCTGCGC CTACCAGGTG TGC

23

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.56 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GGCCTCCCTG ACGCTATGGT TCCAG

25

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCPl.57 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGTGCTGCCG CTGGCCACGT TCG

23

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.58 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TCCCAGGGCA CGCACACCAG GCACT

25

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.59 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTACAGGGCA CACCTTTGGT CACTC

25

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TCGACGACGT ACACACTCAT CAGCC

25

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.61 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCGGCAGCA CCTCGCGGTA GTGGC

25

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.62 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CCACCAGCTC CTTAGGCAG GACAC

25

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.63 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

CCAGGGCTTC CCACGTGCGC AGCAG

25

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.64 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CGCACGAACG TGGCCAGCGG CAGCA

25

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.65 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

TGACCGTGGT TTCTGTGTGG TGT

23

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.66 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

CCCTCTTCAA GTGCTGTCTG ATTCC

25

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCPl.67 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

ATCGCGGCCA CCACGTCCCT

20

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.68 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TGCTCCAGAC ACTCGGCCGG TAGAA

25

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.69 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

ACGAAGCCGT ACACCTGCC

19

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.72 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

CGACATCCCT GCGTTCTTGG CTTTC

25

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.73 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

CACTGCTGGC CTCATTCAGG G

21

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCPl.74 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GCGACATGGA GAACAAGC

18

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCPl.75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GCAGCCATAC TCAGGGACAC

20

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.76 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

CCATCCTCTC CACGCTGCTC

20

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.77 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GCGATGACCT CCGTGAGCCT G

21

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.78 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CCCAGGACAG GCTCACGGA

19

2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCTCTTCAAG TGCTGTCTGA TTCC

24

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "billTCP2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

CAGCTCGACG ACGTACACAC TCATC

25

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "billTCP4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

CTGACGTCCA GACTCCGCTT CAT

23

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "rpprim01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GACCTGAGCA GCTCGACGAC GTACACACTC ATC

33

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Ltl primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCGTCGAGC TGCTCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AGCACGCTGA ACAGTGCCTT

20

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GACCTGAGCA GCTCGACGAC

20

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

AAGGCACTGT TCAGCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CGGCCGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "Lt6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGATGAAGCG GAGTCTGGA

19

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "BamH1Lt7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

ATGGATCCGT CGTCGAGCTG CTCAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "Sal1Lt8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

ATCAGCTGAG CACGCTGAAC AGTGCCTTC

29

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K303 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTCTCCGTGA CATAAAAGAA AGAC

24

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "K304 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GCCAAGTTCC TGCACTGGCT

20

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K305 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K306 primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine substituted by two
biotin groups"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

NCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K311 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GTCAAGATGC CTGAGATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K312 and K313 primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

TGCTTAGCTT GTGGGGGTGT CA

22

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GCTGCGTCCT GCTGCGCACG T

21

(2) INFORMATION FOR SEQ ID NO:469:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K321 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K322 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TGGGCCACCA GCGCGCGGAA A

21

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "slanti.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CGGCCGCAGC CCGTCAGGCT TGGGG

25

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "slanti.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CCGACAGCTC CCGCAGCTGC ACCC

24

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "slanti.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

CGTACACACT CATCAGCCAG TGCAGGA ACT TGGC

34

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "slanti.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

CGCGCCCGCT CGTAGTTGAG CACGCTGAAC AGTGCCTTCA CCCTCG

46

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "slanti.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GCGGAGTCTG GACGTCAGCA GGGCGGGCCT GGCTTCCCG

39

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "UTR2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

ATTTGACCCA CAGGGACCCC CATCCAG

27

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "FW5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

ATGACCGCCC TCCTCGTGAG

20

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Naml primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCACCCCCG CGATGCC

17

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

AGCCCTGGCC CCGGCCA

17

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

TCCCACGTGC GCAGCAG

17

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AGCAGGACGC AGCGCTG

17

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "PE01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CGCGGTAGTG GCTGCGCAGC AGGGAGCGCA CGGC

34

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "PE02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

CCAGGGCTTC CCACGTGCGC AGCAGGACGC AGCGC

35

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "LM101 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

CTAGTCTAGA TCRCTAGCGT AATCTGGAAC ATCGTATGGG TRTCCAGGAT GGTCTTGAAG 60
TC 62

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM103 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TACCATGGGC TACCCATACG ACGTTCCAGA TTACGCTCA 39

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM104 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

TATGAGCGTA ATCTGGAACG TCGTATGGGT AGCCCATGG 39

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /note= "LM105 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GTGTACGTCG TCGAGCTCCT CAGGTCTGCC TTTTATGTCA CGGAG

45

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM106 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GTGTACGTCG TCGAGCTCCT CAGGTCTTTC GCTTATGTCA CGGAGACC

48

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM107 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CCTCAGGTCT TTCTTTGCTG TCACGGAGAC AACGTTTCAA AAGAACAG

48

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "LM108 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGTCTTTCTT TTATGTCGCG GAGACAACGT TTCAAAGAA CAG

43

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: /note= "LM109 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

CTTTCTTTTA TGTCACGGCG ACAACGTTTC AAAAGAACAG

40

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "LM_FFYTE primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

ATGAGTGTGT ACGTCGTCGA GCTCCTCAGG TCTACCACGT TTCAAAAGAA CAGGCTCTTT 60
TTC 63

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP061 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GGCTGATGAG TGTGTACGTC GTCGA 25

(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "HUM01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

ACGTGGTCTC CGTGACATAA AAGAA 25

(2) INFORMATION FOR SEQ ID NO:495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGGTCTTTCT TTTATGTCAC GGA

23

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "HUMO3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

CACAGACCCC CGTCGCCTGG TC

22

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

CGGAGTCTGG ACGTCAGCAG GGC

23

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F1N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CGCGGATCCG TAACTAAAT GCCGCGCGCT CCCCCTGC

39

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F1C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

CCGGAATTCG TTAGTTACTT ACAAAGAGGT GGCTTCTTCG GC

42

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F2N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

CGCGGATCCG TAACTAAAGC CACCTCTTTG GAGGGTGCG

39

(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F2C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

CCGGAATTCG TTAGTTACTT AAGACCTGAG CAGCTCGACG AC

42

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F3N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

CGCGGATCCG TAACTAAAAAT GAGTGTGTAC GTCGTCGAG

39

(2) INFORMATION FOR SEQ ID NO:503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F3C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

CCGGAATTCG TTAGTTACTT AGATCCCCTG GCACTGGACG

40

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F4N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CGCGGATCCG TAACTAAAAT CCCGCAGGGC TCCATCCTC

39

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F4C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

CCGGAATTCG TTAGTTACTT AGTCCAGGAT GGTCTTGAAG TC

42

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "40-60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GGCATCGCGG GGGTGGCCGG G

21

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "260-280 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGACACCTGG CGGAAGGAGG G

21

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "500-520 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GCGTGCCAGC AGGTGAACCA G

21

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "770-790 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTCAGGGGCA GCGCCACGCC T

21

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "885-905 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

AGGTGGCTTC TTCGGCGGGT C

21

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1000-1020 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GGACAAGGCG TGTCCCAGGG A

21

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1300-1320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GCTGGGGTGA CCGCAGCTCG C

21

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1520-1540 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GATGAACTTC TTGGTGTTC T

21

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2110-2130 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GTGCGCCAGG CCCTGTGGAT A

21

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2295-2315 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GCCCATGGGC GGCCTTCTGG A

21

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2450-2470 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAGGCCACTG CTGGCCTCAT T

21

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2670-2690 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGGTGAGGTG AGGTGTCACC A

21

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "3080-3110 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GCTGCAGCAC ACATGCGTGA AACCTGTACG C

31

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3140-3160 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GACGCGCAGG AAAAATGTGG G

21

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3690-3710 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

CCGAGCGCCA GCCTGTGGGG A

21

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "55-75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

CAGCGGGGAG CGCGGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "151-171 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

CAGCACCTCG CGGTAGTGGC T

21

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

TCAAGCCAAA CCTGAATCTG AG

22

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TP1.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

CCCGAGTGAA TCTTTCTACG C

21

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TP1.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GTCTCTGGCA GTTTCCTCAT CCC

23

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

TTTAGGCATC CTCCAAGCA CA

22

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TTAGGGTTAG

10

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

TTAGGGTTAG GGTTAGGG

18

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GTTAGGGTTA GGGTTAGG

18

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (CCCTAA)-n, where n is at least 1, or at least 3, or at least 10 or more"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

CCCTAACCT AACCTAACCT AACCTAACCT AACCTAACCT AACCTAACCT AACCTAACCT AACCTAACCT 60

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAG 34

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN AGGG

34

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG

40

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG GGTTAG

46

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AG

52

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AGGGTTAG

58

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "primer terminating at template boundary"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

TAGGGATTAG

10

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "primer for hTRT nucleolytic assay"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-deoxyguanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TTAGGGTTAG GGTTAN

16

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (TTAGGG)-n, where n is 1-10, or typically 3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

TTAGGGTTAG GGTAGGGTT AGGGTTAGG TTAGGGTTAG GGTAGGGTT AGGGTTAGG

60

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Trp Xaa Gly Xaa Ser
1 5

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Pro Arg Arg Arg
1

67

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Pro Lys Arg Pro Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "antisense hTERT molecule"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GCTCTAGAAT GAAGGGTG

18

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S1 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GGGACGACTG ACATTGGCCG G

21

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S2 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GGCTCGAAGT AGCACCGGTG C

21

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S3 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GTGGGAACAG GCCGATGTCC C

21

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON1 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

TCCCACGTGC GCAGCAGGAC GCAGCGCTGC

30

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON2 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GCCGGGGCCA GGGCTTCCCA CGTGCGCAGC

30

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON3 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCATCGCGG GGGTGGCCGG GGCCAGGGCT

30

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "delta-182 species specific primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GGCACTGGAC GTAGGACGTG

20

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "293 cell line lambda cDNA
 library PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGAAGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /note= "GAPDH control primer K136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

CTCAGACACC ATGGGGAAGG TGA

23

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /note= "GAPDH control primer K137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ATGATCTTGA GGCTGTTGTC ATA

23

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "biotin-labeled
telomerase-specific oligonucleotide"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = thymidine modified by a
biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..13
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 14..17
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18..21
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 22..25
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

NAGACCTGTT ANNNNNNNNNN MNNNNN

26

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "displacement
deoxyoligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: /note= "5' primer encoding a hammerhead ribozyme, a T7-promoter and an EcoR1 site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA 60

ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "3' primer including an EarI site and a BamH1 site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC

36

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

CCCCAAAACC CCAAACCCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

CCAAAACCCCC AAAACCCCCA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAAACCCCCA AACCCCCAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TTGGGG 56

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

AAAACCCCAA AACCCCCACA GGGGTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TCTRAARTAR TGDGTNAORT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

DGCDGTYTCY TGRTCRTTTRT A

21

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K231 forward primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a
biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

NCCTATTTYT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K220 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K228 forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K224 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K227 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: /note= "clone 168-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GATTACTCCC GAAGAAAGGA TCTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K297 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAGTGACATA ATATACGTGA	20
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(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: /note= "Tetrahymena DNA fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT      60
AAATTAACTA TTGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT      120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG      180
ATACCAGAAG ATTCATTTTA GAAATACCCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA      240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA      300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG      360
GGATAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA      420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA          474

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "Q-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT      50

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-O primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GTGTCATTTT TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-I primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "M2-B2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiI primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiII primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "F3b primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TCTAACCCCTA ACTGAGAAGG GCGTAG

26

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "R3c primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GTTTGCTCTA GAATGAACGG TGGAAG

26

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: /note= "104-base intronic sequence (SEQ ID NO:7) inserted at the junction corresponding to bases 274 and 275 of hTRT (SEQ ID NO:1)"

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 28..131
- (D) OTHER INFORMATION: /note= "intronic sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

CCCCCGCCG CCCCCTCCTT CCGCCAGGTG GGCCTCCCCG GGGTCGGCGT CCGGCTGGGG	60
TTGAGGGCGG CCGGGGGGAA CCAGCGACAT GCGGAGAGCA GCGCAGGCGA CTCAGGGCGC	120
TTCCCCCGCA GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG	170

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1285
- (D) OTHER INFORMATION: /note= "fusion protein composed of enterokinase cleavable, His tagged thioredoxin moiety and full length hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met	Ser	Asp	Lys	Ile	Ile	His	Leu	Thr	Asp	Asp	Ser	Phe	Asp	Thr	Asp	1	5	10	15
Val	Leu	Lys	Ala	Asp	Gly	Ala	Ile	Leu	Val	Asp	Phe	Trp	Ala	His	Trp	20	25	30	
Cys	Gly	Pro	Cys	Lys	Met	Ile	Ala	Pro	Ile	Leu	Asp	Glu	Ile	Ala	Asp	35	40	45	
Glu	Tyr	Gln	Gly	Lys	Leu	Thr	Val	Ala	Lys	Leu	Arg	Ile	Asp	His	Asn	50	55	60	
Pro	Gly	Thr	Ala	Pro	Lys	Tyr	Gly	Ile	Arg	Gly	Ile	Pro	Thr	Leu	Leu	65	70	75	80
Leu	Phe	Lys	Asn	Gly	Glu	Val	Ala	Ala	Thr	Lys	Val	Gly	Ala	Leu	Ser	85	90	95	
Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala	Gly	Ser	Gly	100	105	110	
Ser	Gly	Asp	Asp	Asp	Asp	Lys	Val	Pro	Met	His	Glu	Leu	Glu	Ile	Phe	115	120	125	
Glu	Phe	Ala	Ala	Ala	Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp	130	135	140	
Glu	Ala	Leu	Ala	Pro	Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys	145	150	155	160
Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro	165	170	175	
Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val	180	185	190	
Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu	195	200	205	
Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe	210	215	220	
Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	225	230	235	240
Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	245	250	255	
Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	260	265	270	
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	275	280	285	
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	290	295	300	
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	305	310	315	320

Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 325 330 335
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 340 345 350
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 355 360 365
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 370 375 380
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280

Lys Thr Ile Leu Asp
1285

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Gly Ser Val Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
 (B) LOCATION: 1..538
 (D) OTHER INFORMATION: /note= "fusion protein composed of
 glutathione-S-transferase sequence,
 thrombin cleavage sequence, recognition
 sequence for heart muscle protein
 kinase, residues introduced by cloning
 and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	85	90	95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	100	105	110	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	115	120	125	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155	160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220	
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ile	Pro	Gln	Gly	225	230	235	240
Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	245	250	255	
Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	260	265	270	
Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr	275	280	285	
Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	290	295	300	
Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	305	310	315	320
Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	325	330	335	
Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	340	345	350	
Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Val	Thr	Phe	Asn	Arg	355	360	365	
Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	370	375	380	
Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	385	390	395	400

Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr
 405 410 415
 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430
 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445
 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460
 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480
 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495
 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510
 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525
 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning, eight consecutive His residues and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	50	55	60
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	65	70	75
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	85	90	95
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	100	105	110
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	115	120	125
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	His	His	His	His	His	His	225	230	235
His	His	Gly	Ser	Val	Thr	Lys	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	245	250	255
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	260	265	270
Phe	Phe	Tyr	Arg	Pro	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	275	280	285
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	290	295	300
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	305	310	315
Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	325	330	335
Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	340	345	350
Leu	Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	355	360	365

Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380

Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415

Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430

Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445

Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460

Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480

Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495

Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510

Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525

Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTERT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Ser Val Tyr
 225 230 235 240
 Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
 245 250 255
 Gln Lys Asn Arg Leu Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu
 260 265 270
 Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
 275 280 285
 Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
 290 295 300
 Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
 305 310 315 320
 Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
 325 330 335

Lys Arg Ala Glu Arg Leu Thr Ser Arg Lys Ala Leu Phe Ser Val Leu
 340 345 350
 Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu
 355 360 365
 Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val
 370 375 380
 Arg Ala Gln Asp Pro Pro Pro Glu Tyr Phe Val Lys Val Asp Val Thr
 385 390 395 400
 Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430
 Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445
 Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460
 Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480
 Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510
 Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ala Thr Ser Leu
 225 230 235 240
 Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 245 250 255
 Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 260 265 270
 Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 275 280 285
 Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 290 295 300
 Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 305 310 315 320

Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 325 330 335
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 340 345 350
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 355 360 365
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 370 375 380
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 385 390 395 400
 Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 405 410 415
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTERT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Pro Arg Ala
 225 230 235 240
 Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Ser His Tyr Arg Glu Val
 245 250 255
 Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg
 260 265 270
 Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln
 275 280 285
 Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro Ala Ala Pro Ser
 290 295 300
 Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln
 305 310 315 320

Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala
 325 330 335
 Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Thr Thr Ser Val
 340 345 350
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 355 360 365
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 370 375 380
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Cys Ala Tyr
 385 390 395 400
 Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala
 405 410 415
 Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu
 420 425 430
 Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu
 435 440 445
 Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu
 450 455 460
 Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg
 465 470 475 480
 Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly
 485 490 495
 Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
 500 505 510
 Glu Ala Thr Ser Leu
 515

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "oligonucleotide used to modify hTERT cDNA nucleotides 779 to 781 from GCG to CAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CCGGCCACCC CCCATATGCC GCGCGCTCCC

30

(2) INFORMATION FOR SEQ ID NO:608:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN127, pGRN128 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCTG

58

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN129 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC

60

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1154
- (D) OTHER INFORMATION: /note= "fusion protein composed of hTRT protein sequence, vector sequences, the Myc epitope and His6 tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
 1125 1130 1135

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 1140 1145 1150

His His

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hTERT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met	Pro	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	1	5	10	15
Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Leu	20	25	30	
Asp	Pro	Ser	Ser	Arg	Ser	Ala	Ala	Gly	Thr	Met	Glu	Phe	Ala	Ala	Ala	35	40	45	
Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp	Glu	Ala	Leu	Ala	Pro	50	55	60	
Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	65	70	75	80
Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	85	90	95	
Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	100	105	110	
Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	115	120	125	
Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	130	135	140	
Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	145	150	155	160
Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	165	170	175	

Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	180	185	190	
Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	195	200	205	
Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	210	215	220	
Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	225	230	235	240
Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	245	250	255	
His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	260	265	270	
His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	275	280	285	
Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	290	295	300	
Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	305	310	315	320
Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	325	330	335	
Gly	Phe	Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	340	345	350	
Leu	Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	355	360	365	
Arg	Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	370	375	380	
Trp	Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	385	390	395	400
Tyr	Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	405	410	415	
Ser	Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	420	425	430	
Phe	Leu	Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	435	440	445	
Arg	Leu	Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	450	455	460	
Leu	Gly	Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	465	470	475	480
Cys	Pro	Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	485	490	495	

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1170 1175 1180
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1189
- (D) OTHER INFORMATION: /note= "fusion protein composed of
 melittin signal sequence and full length
 hTRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15
 Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met
 20 25 30
 Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 35 40 45
 Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 50 55 60
 Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 65 70 75 80
 Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 85 90 95
 Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 100 105 110
 Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 115 120 125
 Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 130 135 140

Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 145 150 155 160
 Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 165 170 175
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 180 185 190
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 195 200 205
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 210 215 220
 Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 225 230 235 240
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 245 250 255
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460

Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780

Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100

Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
1105 1110 1115 1120

Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
1125 1130 1135

Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
1140 1145 1150

Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
1155 1160 1165

Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
1170 1175 1180

Lys Thr Ile Leu Asp
1185

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..92
(D) OTHER INFORMATION: /note= "oligonucleotide used to create
expression vectors pGRN128 and pGRN129"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

CTGCCCCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTCAG 60
ATCTGCGGGC GCCACCGCGG TGGAGCTCCA GC 92

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..53
(D) OTHER INFORMATION: /note= "mutagenic oligo used to add a CSP45I site at the C-terminus of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCCGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "oligonucleotide RA45"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GCCACCCCCG CGCTGCCTCG AGCTCCCCGC TGC

33

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "primer hTR+1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "primer hTR+445"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "synthetic telomerase product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

ATTCGTCGA GCAGAGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT

60

AG

62

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer H3.03"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TTAGGGTTAG GGTTAGGG

18

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

AATCCGTCSA GCAGAGGG

18

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

AATCCGTCSA GCAGATAG

18

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T701 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGC 60
TCCCACGACG TAGTCCATGT TCAC 84

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "reverse01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGGTCTAGAT CCGGAAGAGT GTCTGGAGCA AG 32

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T702 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGG 60
CGGCCTTCTG GACCACGGCA TACC 84

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "reverse02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGTCTAGACG ATATCCACAG GGCCTGGCGC

30

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1407
- (D) OTHER INFORMATION: /note= "fusion protein composed of enhanced green fluorescent protein (EGFP) residues, residues encoded by the 5' untranslated region of hTRT mRNA and hTRT protein sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Arg Thr Gln Ile Ser Ser Ser Ser Phe Glu Phe Ala Ala Ala Ser
 245 250 255
 Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala
 260 265 270
 Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu
 275 280 285
 Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg
 290 295 300
 Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala
 305 310 315 320
 Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp
 325 330 335
 Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu
 340 345 350
 Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala
 355 360 365
 Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly
 370 375 380
 Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn
 385 390 395 400

Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu
 405 410 415
 Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala
 420 425 430
 Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro
 435 440 445
 Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His
 450 455 460
 Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His
 465 470 475 480
 Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala
 485 490 495
 Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg
 500 505 510
 Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln
 515 520 525
 Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly
 530 535 540
 Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu
 545 550 555 560
 Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 565 570 575
 Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 580 585 590
 Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 595 600 605
 Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 610 615 620
 Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 625 630 635 640
 Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 645 650 655
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 660 665 670
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 675 680 685
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 690 695 700
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 705 710 715 720

Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 725 730 735
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 740 745 750
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 755 760 765
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 770 775 780
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 785 790 795 800
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 805 810 815
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 820 825 830
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 835 840 845
 Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 850 855 860
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 865 870 875 880
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 885 890 895
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 900 905 910
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 915 920 925
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 930 935 940
 Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 945 950 955 960
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 965 970 975
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 980 985 990
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 995 1000 1005
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 1010 1015 1020
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 1025 1030 1035 1040

Leu Thr Asp	Leu Gln Pro Tyr Met Arg	Gln Phe Val Ala His	Leu Gln
	1045	1050	1055
Glu Thr Ser	Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser		
	1060	1065	1070
Leu Asn Glu Ala Ser Ser Gly	Leu Phe Asp Val Phe	Leu Arg Phe Met	
	1075	1080	1085
Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln			
	1090	1095	1100
Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr	Leu Leu Cys Ser Leu Cys		
	1105	1110	1115 1120
Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly			
	1125	1130	1135
Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu			
	1140	1145	1150
Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu			
	1155	1160	1165
Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val			
	1170	1175	1180
Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His			
	1185	1190	1195 1200
Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu			
	1205	1210	1215
Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser			
	1220	1225	1230
Val Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys			
	1235	1240	1245
Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu			
	1250	1255	1260
Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu			
	1265	1270	1275 1280
Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe			
	1285	1290	1295
His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser			
	1300	1305	1310
Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly			
	1315	1320	1325
Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala			
	1330	1335	1340
Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His			
	1345	1350	1355 1360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: -
(B) LOCATION: 1..18
(D) OTHER INFORMATION: /note= "TS primer"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- ```
(A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "ACX primer"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCGCGGCTTA CCCTTACCCT TACCCTAACC

30

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "U2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

ATCGCTTCTC GGCCTTTT

18

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "TSU2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AATCCGTCGA GCAGAGTTAA AAGGCCGAGA AGCGAT

36

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Cys Tyr Asp Xaa
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

Lys Xaa Tyr Xaa Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser
 1 5 10 15

Xaa Xaa Leu

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Leu Leu Arg Leu Xaa Asp Asp Xaa Leu Xaa Ile Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing
alternative codon distributions for
E. coli (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

ATGCCGCGCG CGCCGCGCTG CCGCGCGGTG CGCAGCCTGC TGCGCAGCCA TTATCGCGAA	60
GTGCTGCCGC TGGCGACCTT TGTGCGCCGC CTGGGCCCCG AGGGCTGGCG CCTGGTGCAG	120
CGCGGCGATC CGGCGGCGTT TCGCGCGCTG GTGGCGCAGT GCCTGGTGTG CGTGCCGTGG	180
GATGCGCGCC CGCCGCCGGC GCGCGCGAGC TTTGCCCAGG TGAGCTGCCT GAAAGAACTG	240
GTGGCGCGCG TGCTGCAGCG CCTGTGCGAA CGCGGCGCGA AAAACGTGCT GGCCTTTGGC	300
TTTGCGCTGC TGGATGGCGC GCGCGGCGGC CCGCCGGAAG CGTTTACCAC CAGCGTGC GC	360
AGCTATCTGC CGAACACCGT GACCGATGCG CTGCGCGGCA GCGGCGCGTG GGGCCTGCTG	420
CTGCGCCGCG TGGGCGATGA TGTGCTGGTG CATCTGCTGG CGCGCTGCGC GCTGTTTGTG	480
CTGGTGGCGC CGAGCTGCGC GTATCAGGTG TGCGGCCCCG CGCTGTATCA GCTGGGCGCG	540
GCGACCCAGG CGCGCCCGCC GCCGCATGCG AGCGGCCCCG GCCGCCGCCT GGGCTGCGAA	600
CGCGCGTGGA ACCATAGCGT GCGCGAAGCG GGCCTGCCGC TGGGCCTGCC GCGCGCGGGC	660
GCGCGCCGCC GCGGCGGCAG CGCGAGCCGC AGCCTGCCGC TGCCGAAACG CCCGCGCCGC	720
GGCGCGGCGC CGGAACCGGA ACGCACCCCG GTGGGCCAGG GCAGCTGGGC GCATCCGGGC	780
CGCACCCGCG GCCCGAGCGA TCGCGGCTTT TCGTGGTGA GCCCGGCGCG CCCGGCGGAA	840
GAAGCGACCA GCCTGGAAGG CGCGCTGAGC GGCACCCGCC ATAGCCATCC GAGCGTGGGC	900
CGCCAGCATC ATGCGGGCCC GCCGAGCACC AGCCGCCCGC CGCGCCCGTG GGATACCCCG	960
TGCCCCCGCG TGTATGCGGA AACCAAACAT TTTCTGTATA GCAGCGGCGA TAAAGAACAG	1020
CTGCGCCCGA GCTTTCTGCT GAGCAGCCTG CGCCCGAGCC TGACCGGCGC GCGCCGCCTG	1080
GTGGAAACCA TTTTCTGGG CAGCCGCCCG TGGATGCCGG GCACCCCGCG CCGCCTGCCG	1140
CGCCTGCCGC AGCGCTATTG GCAGATGCGC CCGCTGTTTC TGGAAGTCT GGGCAACCAT	1200
GCGCAGTGCC CGTATGGCGT GCTGCTGAAA ACCCATTGCC CGCTGCGCGC GCGGGTGACC	1260
CCGGCGGCGG GCGTGTGCGC GCGCGAAAAA CCGCAGGGCA GCGTGGCGGC GCCGGAAGAA	1320
GAAGATACCG ATCCGCGCCG CCTGGTGCAG CTGCTGCGCC AGCATAGCAG CCCGTGGCAG	1380
GTGTATGGCT TTGTGCGCGC GTGCCTGCGC CGCCTGGTGC CGCCGGGCCT GTGGGGCAGC	1440
CGCCATAACG AACGCCGCTT TCTGCGCAAC ACCAAAAAAT TTATTAGCCT GGGCAAACAT	1500
GCGAAACTGA GCCTGCAGGA ACTGACCTGG AAAATGAGCG TGCGCGATTG CGCGTGGCTG	1560
CGCCGCAGCC CGGGCGTGGG CTGCGTGCCG GCGGCGGAAC ATCGCCTGCG CGAAGAAATT	1620
CTGGCGAAAT TTCTGCATTG GCTGATGAGC GTGTATGTGG TGGAAGTCT GCGCAGCTTT	1680
TTTTATGTGA CCGAAACCAC CTTTCAGAAA AACCGCCTGT TTTTTTATCG CAAAAGCGTG	1740
TGGAGCAAAC TGCAGAGCAT TGGCATTGCG CAGCATCTGA AACGCGTGCA GCTGCGCGAA	1800

CTGAGCGAAG CGGAAGTGCG CCAGCATCGC GAAGCGCGCC CGGCGCTGCT GACCAGCCGC	1860
CTGCGCTTTA TTCCGAAACC GGATGGCCTG CGCCCATTG TGAACATGGA TTATGTGGTG	1920
GGCGCGCGCA CCTTTCGCCG CGAAAAACGC GCGGAACGCC TGACCAGCCG CGTGAAAGCG	1980
CTGTTTAGCG TGCTGAACTA TGAACGCGCG CGCCGCCCGG GCCTGCTGGG CGCGAGCGTG	2040
CTGGGCCTGG ATGATATTCA TCGCGCGTGG CGCACCTTG TGCTGCGCGT GCGCGCGCAG	2100
GATCCGCCGC CGGAACTGTA TTTTGTGAAA GTGGATGTGA CCGGCGCGTA TGATACCATT	2160
CCGCAGGATC GCCTGACCGA AGTGATTGCG AGCATTATTA AACCAGAGAA CACCTATTGC	2220
GTGCGCCGCT ATGCGGTGGT GCAGAAAGCG GCGCATGGCC ATGTGCGCAA AGCGTTTAAA	2280
AGCCATGTGA GCACCCTGAC CGATCTGCAG CCGTATATGC GCCAGTTTGT GGCGCATCTG	2340
CAGGAAACCA GCCCGCTGCG CGATGCGGTG GTGATTGAAC AGAGCAGCAG CCTGAACGAA	2400
GCGAGCAGCG GCCTGTTTGA TGTGTTTCTG CGCTTTATGT GCCATCATGC GGTGCGCATT	2460
CGCGGCAAAA GCTATGTGCA GTGCCAGGGC ATTCGCGAGG GCAGCATTCT GAGCACCTG	2520
CTGTGCAGCC TGTGCTATGG CGATATGGAA AACAACTGT TTGCGGGCAT TCGCCGCGAT	2580
GGCCTGCTGC TGCGCCTGGT GGATGATTTT CTGCTGGTGA CCCCAGCATCT GACCCATGCG	2640
AAAACCTTTC TGCGCACCTT GGTGCGCGGC GTGCCGGAAT ATGGCTGCGT GGTGAACCTG	2700
CGCAAAACCG TGGTGAACCT TCCGGTGGAA GATGAAGCGC TGGGCGGCAC CGCGTTTGTG	2760
CAGATGCCGG CGCATGGCCT GTTTCGCTGG TGCGGCCTGC TGCTGGATAC CCGCACCTG	2820
GAAGTGCAGA GCGATTATAG CAGCTATGCG CGCACCAGCA TTCGCGCGAG CCTGACCTTT	2880
AACCGCGGCT TTAAAGCGGG CCGCAACATG CGCCGCAAAC TGTTTGGCGT GCTGCGCCTG	2940
AAATGCCATA GCCTGTTTCT GGATCTGCAG GTGAACAGCC TGCAGACCGT GTGCACCAAC	3000
ATTTATAAAA TTCTGCTGCT GCAGGCGTAT CGCTTTCATG CGTGCGTGCT GCAGCTGCCG	3060
TTTCATCAGC AGGTGTGGAA AAACCCGACC TTTTTCTGC GCGTGATTAG CGATACCGCG	3120
AGCCTGTGCT ATAGCATTCT GAAAGCGAAA AACGCGGGCA TGAGCCTGGG CGCGAAAGGC	3180
GCGGCGGGCC CGCTGCCGAG CGAAGCGGTG CAGTGGCTGT GCCATCAGGC GTTCTGCTG	3240
AAACTGACCC GCCATCGCGT GACCTATGTG CCGCTGCTGG GCAGCCTGCG CACCGCGCAG	3300
ACCCAGCTGA GCCGCAAAC TCCGGGCACC ACCCTGACCG CGCTGGAAGC GGCGGCGAAC	3360
CCGGCGCTGC CGAGCGATTT TAAAACCATT CTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for enteric bacteria (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

ATGCCGCGTG CTCCGCGTTG CCGTGCTGTT CGTTCCCTGC TCGGTTCCCA CTACCGTGAA	60
GTTCTGCCGC TGGCTACCTT CGTTCGTCGT CTGGGTCCGC AGGGTTGGCG TCTGGTTCAG	120
CGTGGTGACC CGGCTGCTTT CCGTGCTCTG GTTGCTCAGT GCCTGGTTTG CGTTCCGTGG	180
GACGCTCGTC CGCCGCCGGC TGCTCCGTCC TTCCGTCAGG TTTCCTGCCT GAAAGAACTG	240
GTTGCTCGTG TTCTGCAGCG TCTGTGCGAA CGTGGTGCTA AAAACGTTCT GGCTTTCGGT	300
TTCGCTCTGC TGGACGGTGC TCGTGGTGGT CCGCCGGAAG CTTTCACCAC CTCCGTTCGT	360
TCCTACCTGC CGAACACCGT TACCGACGCT CTGCGTGGTT CCGGTGCTTG GGGTCTGCTG	420
CTGCGTCGTG TTGGTGACGA CGTTCTGGTT CACCTGCTGG CTCGTTGCGC TCTGTTTCGT	480
CTGGTTGCTC CGTCTGCGC TTACCAGGTT TGCGGTCCGC CGCTGTACCA GCTGGGTGCT	540
GCTACCCAGG CTCGTCCGCC GCCGCACGCT TCCGGTCCGC GTCGTGCTCT GGGTTGCGAA	600
CGTGCTTGGA ACCACTCCGT TCGTGAAGCT GGTGTTCCGC TGGGTCTGCC GGCTCCGGGT	660
GCTCGTCGTC GTGGTGGTTC CGCTTCCCGT TCCCTGCCGC TGCCGAAACG TCCGCGTCGT	720
GGTGCTGCTC CGGAACCGGA ACGTACCCCG GTTGGTCAGG GTTCCTGGGC TCACCCGGGT	780
CGTACCCGTG GTCCGTCCGA CCGTGGTTTC TGCCTTGTTT CCCC GGCTCG TCCGGCTGAA	840
GAAGCTACCT CCCTGGAAGG TGCTCTGTCC GGTACCCGTC ACTCCCACCC GTCCGTTGGT	900
CGTCAGCACC ACGCTGGTCC GCCGTCCACC TCCCGTCCGC CGCGTCCGTG GGACACCCCG	960
TGCCCCGCCG TTTACGCTGA AACCAAACAC TTCCTGTACT CCTCCGGTGA CAAAGAACAG	1020
CTGCGTCCGT CCTTCCTGCT GTCCTCCCTG CGTCCGTCCC TGACCGGTGC TCGTCGTCTG	1080
GTTGAAACCA TCTTCCTGGG TTCCCGTCCG TGGATGCCGG GTACCCCGCG TCGTCTGCCG	1140
CGTCTGCCGC AGCGTTACTG GCAGATGCGT CCGCTGTTCC TGGAAGTCT GGGTAACCAC	1200

GCTCAGTGCC CGTACGGTGT TCTGCTGAAA ACCCACTGCC CGCTGCGTGC TGCTGTTACC	1260
CCGGCTGCTG GTGTTTGCGC TCGTGAAAAA CCGCAGGGTT CCGTTGCTGC TCCGGAAGAA	1320
GAAGACACCG ACCCGCGTCG TCTGGTTCAG CTGCTGCGTC AGCACTCCTC CCCGTGGCAG	1380
GTTTACGGTT TCGTTCGTGC TTGCCTGCGT CGTCTGGTTC CGCCGGGTCT GTGGGGTTCC	1440
CGTCACAACG AACGTCGTTT CCTGCGTAAC ACCAAAAAAT TCATCTCCCT GGGTAAACAC	1500
GCTAAACTGT CCCTGCAGGA ACTGACCTGG AAAATGTCCG TTCGTGACTG CGCTTGGCTG	1560
CGTCGTTCCC CGGGTGTTGG TTGCGTTCCG GCTGCTGAAC ACCGTCTGCG TGAAGAAATC	1620
CTGGCTAAAT TCCTGCACTG GCTGATGTCC GTTTACGTTG TTGAACTGCT GCGTTCCTTC	1680
TTCTACGTTA CCGAAACCAC CTTCCAGAAA AACCGTCTGT TCTTCTACCG TAAATCCGTT	1740
TGGTCCAAAC TGCAGTCCAT CGGTATCCGT CAGCACCTGA AACGTGTTCA GCTGCGTGAA	1800
CTGTCCGAAG CTGAAGTTCG TCAGCACCGT GAAGCTCGTC CGGCTCTGCT GACCTCCCGT	1860
CTGCGTTTCA TCCCGAAACC GGACGGTCTG CGTCCGATCG TTAACATGGA CTACGTTGTT	1920
GGTGCTCGTA CCTTCCGTGC TGAAAAACGT GCTGAACGTC TGACCTCCCG TGTTAAAGCT	1980
CTGTTCTCCG TTCTGAACTA CGAACGTGCT CGTCGTCCGG GTCTGCTGGG TGCTTCCGTT	2040
CTGGGTCTGG ACGACATCCA CCGTGCTTGG CGTACCTTCG TTCTGCGTGT TCGTGCTCAG	2100
GACCCGCCGC CGGAACTGTA CTTTCGTTAAA GTTGACGTTA CCGGTGCTTA CGACACCATC	2160
CCGCAGGACC GTCTGACCGA AGTTATCGCT TCCATCATCA AACCGCAGAA CACCTACTGC	2220
GTTCGTCGTT ACGCTGTTGT TCAGAAAGCT GCTCACGGTC ACGTTTCGTAA AGCTTTCAAA	2280
TCCCACGTTT CCACCCTGAC CGACCTGCAG CCGTACATGC GTCAGTTCGT TGCTCACCTG	2340
CAGGAAACCT CCCCCTGCG TGACGCTGTT GTTATCGAAC AGTCCTCCTC CCTGAACGAA	2400
GCTTCCTCCG GTCTGTTCTGA CGTTTTCTG CGTTTCATGT GCCACCACGC TGTTTCGTATC	2460
CGTGGTAAAT CCTACGTTCA GTGCCAGGGT ATCCCGCAGG GTTCCATCCT GTCCACCCTG	2520
CTGTGCTCCC TGTGCTACGG TGACATGGAA AACAACTGT TCGCTGGTAT CCGTCGTGAC	2580
GGTCTGCTGC TGCGTCTGGT TGACGACTTC CTGCTGGTTA CCCCACCT GACCCACGCT	2640
AAAACCTTCC TGCGTACCCT GGTTCGTGGT GTTCCGGAAT ACGGTTGCGT TGTTAACCTG	2700
CGTAAAACCG TTGTAACTT CCCGGTTGAA GACGAAGCTC TGGGTGGTAC CGCTTTCGTT	2760
CAGATGCCGG CTCACGGTCT GTTCCCGTGG TCGGTCTGC TGCTGGACAC CCGTACCCTG	2820
GAGTTCAGT CCGACTACTC CTCCTACGCT CGTACCTCCA TCCGTGCTTC CCTGACCTTC	2880
AACCGTGGTT TCAAAGCTGG TCGTAACATG CGTCGTAAAC TGTTCCGGTGT TCTGCGTCTG	2940
AAATGCCACT CCCTGTTTCT GGACCTGCAG GTTAACTCCC TGCAGACCGT TTGCACCAAC	3000
ATCTACAAAA TCCTGCTGCT GCAGGCTTAC CGTTTCCACG CTTGCGTTCT GCAGCTGCCG	3060

TTCCACCAGC AGGTTTGGAA AAACCCGACC TTCTTCCTGC GTGTTATCTC CGACACCGCT	3120
TCCCTGTGCT ACTCCATCCT GAAAGCTAAA AACGCTGGTA TGTCCCTGGG TGCTAAAGGT	3180
GCTGCTGGTC CGCTGCCGTC CGAAGCTGTT CAGTGGCTGT GCCACCAGGC TTTCCTGCTG	3240
AAACTGACCC GTCACCGTGT TACCTACGTT CCGCTGCTGG GTTCCCTGCG TACCGCTCAG	3300
ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC	3360
CCGGCTCTGC CGTCCGACTT CAAAACCATC CTGGAC	3396

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTTGT TGAGATCTCA TTATAGAGAA	60
GTTTTGCCAT TGGCTACTTT TGTTAGAAGA TTGGGTCCAC AAGGTTGGAG ATTGGTTCAA	120
AGAGGTGATC CAGCTGCTTT TAGAGCTTTG GTTGCTCAAT GTTTGGTTTG TGTTCCATGG	180
GATGCTAGAC CACCACCAGC TGCTCCATCT TTTAGACAAG TTTCTTGTTT GAAAGAATTG	240
GTTGCTAGAG TTTTGCAAAG ATTGTGTGAA AGAGGTGCTA AAAATGTTTT GGCTTTTGGT	300
TTTGCTTTGT TGGATGGTGC TAGAGGTGGT CCACCAGAAG CTTTTACTAC TTCTGTTAGA	360
TCTTATTTGC CAAATACTGT TACTGATGCT TTGAGAGGTT CTGGTGCTTG GGGTTTGTTG	420
TTGAGAAGAG TTGGTGATGA TGTTTTGGTT CATTTGTTGG CTAGATGTGC TTTGTTTGTT	480
TTGGTTGCTC CATCTTGTGC TTATCAAGTT TGTGGTCCAC CATTGTATCA ATTGGGTGCT	540
GCTACTCAAG CTAGACCACC ACCACATGCT TCTGGTCCAA GAAGAAGATT GGGTTGTGAA	600
AGAGCTTGGA ATCATTTCTGT TAGAGAAGCT GGTGTTCCAT TGGGTTTGCC AGCTCCAGGT	660
GCTAGAAGAA GAGGTGGTTC TGCTTCTAGA TCTTTGCCAT TGCCAAAAAG ACCAAGAAGA	720
GGTGCTGCTC CAGAACCAGA AAGAACTCCA GTTGGTCAAG GTTCTTGGGC TCATCCAGGT	780
AGAACTAGAG GTCCATCTGA TAGAGGTTTT TGTGTTGTTT CTCCAGCTAG ACCAGCTGAA	840

GAAGCTACTT CTTTGGAAGG TGCTTTGTCT GGTACTAGAC ATTCTCATCC ATCTGTTGGT	900
AGACAACATC ATGCTGGTCC ACCATCTACT TCTAGACCAC CAAGACCATG GGATACTCCA	960
TGTCCACCAG TTTATGCTGA AACTAAACAT TTTTGTATT CTTCTGGTGA TAAAGAACAA	1020
TTGAGACCAT CTTTTTTGTT GTCTTCTTTG AGACCATCTT TGA CTGGTGC TAGAAGATTG	1080
GTTGAAACTA TTTTTTTGGG TTCTAGACCA TGGATGCCAG GTACTCCAAG AAGATTGCCA	1140
AGATTGCCAC AAAGATATTG GCAAATGAGA CCATTGTTTT TGAATTGTT GGGTAATCAT	1200
GCTCAATGTC CATATGGTGT TTTGTTGAAA ACTCATTGTC CATTGAGAGC TGCTGTTACT	1260
CCAGCTGCTG GTGTTTGTGC TAGAGAAAAA CCACAAGGTT CTGTTGCTGC TCCAGAAGAA	1320
GAAGATACTG ATCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACATTCTTC TCCATGGCAA	1380
GTTTATGGTT TTGTTAGAGC TTGTTTGAGA AGATTGGTTC CACCAGGTTT GTGGGGTTCT	1440
AGACATAATG AAAGAAGATT TTTGAGAAAT ACTAAAAAT TTATTTCTTT GGGTAAACAT	1500
GCTAAATTGT CTTTGCAAGA ATTGACTTGG AAAATGTCTG TTAGAGATTG TGCTTGGTTG	1560
AGAAGATCTC CAGGTGTTGG TTGTGTTCCA GCTGCTGAAC ATAGATTGAG AGAAGAAATT	1620
TTGGCTAAAT TTTTGCATTG GTTGATGTCT GTTTATGTTG TTGAATTGTT GAGATCTTTT	1680
TTTTATGTTA CTGAAACTAC TTTTCAAAAA AATAGATTGT TTTTTATAG AAAATCTGTT	1740
TGGTCTAAAT TGCAATCTAT TGGTATTAGA CAACATTTGA AAAGAGTTCA ATTGAGAGAA	1800
TTTCTGAAG CTGAAGTTAG ACAACATAGA GAAGCTAGAC CAGCTTTGTT GACTTCTAGA	1860
TTGAGATTTA TTCCAAAACC AGATGGTTTG AGACCAATTG TTAATATGGA TTATGTTGTT	1920
GGTGCTAGAA CTTTTAGAAG AGAAAAAGA GCTGAAAGAT TGA CTCTAG AGTTAAAGCT	1980
TTGTTTTCTG TTTTGAATTA TGAAAGAGCT AGAAGACCAG GTTTGTTGGG TGCTTCTGTT	2040
TTGGGTTTGG ATGATATTCA TAGAGCTTGG AGAACTTTTG TTTTGAGAGT TAGAGCTCAA	2100
GATCCACCAC CAGAATTGTA TTTTGTTAAA GTTGATGTTA CTGGTGCTTA TGATACTATT	2160
CCACAAGATA GATTGACTGA AGTTATTGCT TCTATTATTA AACCACAAAA TACTTATTGT	2220
GTTAGAAGAT ATGCTGTTGT TCAAAAAGCT GCTCATGGTC ATGTTAGAAA AGCTTTTAAA	2280
TCTCATGTTT CTACTTTGAC TGATTTGCAA CCATATATGA GACAATTTGT TGCTCATTTG	2340
CAAGAACTT CTCCATTGAG AGATGCTGTT GTTATTGAAC AATCTTCTTC TTTGAATGAA	2400
GCTTCTTCTG GTTTGTTTGA TGTTTTTTTG AGATTTATGT GTCATCATGC TGTTAGAATT	2460
AGAGGTAAAT CTTATGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTTT GTCTACTTTG	2520
TTGTGTTCTT TGTGTTATGG TGATATGGAA AATAAATTGT TTGCTGGTAT TAGAAGAGAT	2580
GGTTTGTGTT TGAGATTGGT TGATGATTTT TTGTTGGTTA CTCCACATTT GACTCATGCT	2640
AAAAC TTTT TGAGAACTTT GGTTAGAGGT GTTCCAGAAT ATGGTTGTGT TGTTAATTTG	2700

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AGAAAACTG TTGTTAATTT TCCAGTTGAA GATGAAGCTT TGGGTGGTAC TGCTTTTGTT 2760
CAAATGCCAG CTCATGGTTT GTTTCATGG TGTGGTTTGT TGTTGGATAC TAGAACTTTG 2820
GAAGTTCAAT CTGATTATTC TTCTTATGCT AGAACTTCTA TTAGAGCTTC TTTGACTTTT 2880
AATAGAGGTT TTAAAGCTGG TAGAAATATG AGAAGAAAAT TGTTTGGTGT TTTGAGATTG 2940
AAATGTCATT CTTTGTTTTT GGATTGCAA GTTAATTCTT TGCAAAGTGT TTGTACTAAT 3000
ATTTATAAAA TTTTGTTGTT GCAAGCTTAT AGATTTTCATG CTTGTGTTTT GCAATTGCCA 3060
TTTCATCAAC AAGTTTGGA AAATCCAACT TTTTTTTTGA GAGTTATTTT TGATACTGCT 3120
TCTTTGTGTT ATTCTATTTT GAAAGCTAAA AATGCTGGTA TGTCTTTGGG TGCTAAAGGT 3180
GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCATCAAGC TTTTTGTG 3240
AAATTGACTA GACATAGAGT TACTTATGTT CCATTGTTGG GTTCTTTGAG AACTGCTCAA 3300
ACTCAATTGT CTAGAAAATT GCCAGGTACT ACTTTGACTG CTTTGAAGC TGCTGCTAAT 3360
CCAGCTTGC CATCTGATTT TAAACTATT TTGGAT 3396

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(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

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ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTGT TGAGATCTCA CTACAGAGAA 60
GTTTTGCCAT TGGCTACTTT CGTTAGAAGA TTGGGTCCAC AAGGTTGGAG ATTGGTTCAA 120
AGAGGTGACC CAGCTGCTTT CAGAGCTTTG GTTGCTCAAT GTTTGGTTTG TGTTCCATGG 180
GACGCTAGAC CACCACCAGC TGCTCCATCT TTCAGACAAG TTTCTTGTTT GAAGGAATTG 240
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TTGCTTTTGT TGGACGGTGC TAGAGGTGGT CCACCAGAAG CTTTCACTAC TTCTGTTAGA 360
TCTTACTTGC CAAACACTGT TACTGACGCT TTGAGAGGTT CTGGTGCTTG GGGTTTGTTG 420
TTGAGAAGAG TTGGTGACGA CGTTTTGGTT CACTTGTTGG CTAGATGTGC TTTGTTTCGT 480

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GCTACTCAAG CTAGACCACC ACCACACGCT TCTGGTCCAA GAAGAAGATT GGGTTGTGAA	600
AGAGCTTGGG ACCACTCTGT TAGAGAAGCT GGTGTTCCAT TGGGTTTGCC AGCTCCAGGT	660
GCTAGAAGAA GAGGTGGTTC TGCTTCTAGA TCTTTGCCAT TGCCAAAGAG ACCAAGAAGA	720
GGTGCTGCTC CAGAACCAGA AAGAACTCCA GTTGGTCAAG GTTCTTGGGC TCACCCAGGT	780
AGAAGTAGAG GTCCATCTGA CAGAGGTTTC TGTGTTGTTT CTCCAGCTAG ACCAGCTGAA	840
GAAGCTACTT CTTTGGAAGG TGCTTTGTCT GGTACTAGAC ACTCTCACC ATCTGTTGGT	900
AGACAACACC ACGCTGGTCC ACCATCTACT TCTAGACCAC CAAGACCATG GGACACTCCA	960
TGTCCACCAG TTTACGCTGA AACTAAGCAC TTCTTGACTT CTTCTGGTGA CAAGGAACAA	1020
TTGAGACCAT CTTTCTTGTT GTCTTCTTTG AGACCATCTT TGAAGATTG TAGAAGATTG	1080
GTTGAAACTA TTTTCTTGGG TTCTAGACCA TGGATGCCAG GTACTCCAAG AAGATTGCCA	1140
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GCTCAATGTC CATACGGTGT TTTGTTGAAG ACTCACTGTC CATTGAGAGC TGCTGTTACT	1260
CCAGCTGCTG GTGTTTGTGC TAGAGAAAAG CCACAAGGTT CTGTTGCTGC TCCAGAAGAA	1320
GAAGACACTG ACCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACACTCTT TCCATGGCAA	1380
GTTTACGGTT TCGTTAGAGC TTGTTTGAGA AGATTGGTTC CACCAGGTTT GTGGGGTTCT	1440
AGACACAACG AAAGAAGATT CTTGAGAAAC ACTAAGAAGT TCATTTCTTT GGGTAAGCAC	1500
GCTAAGTTGT CTTTGCAAGA ATTGACTTGG AAGATGTCTG TTAGAGACTG TGCTTGGTTG	1560
AGAAGATCTC CAGGTGTTGG TTGTGTTCCA GCTGCTGAAC ACAGATTGAG AGAAGAAATT	1620
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TTGTCTGAAG CTGAAGTTAG ACAACACAGA GAAGCTAGAC CAGCTTTGTT GACTTCTAGA	1860
TTGAGATTCA TTCCAAAGCC AGACGGTTTG AGACCAATTG TTAACATGGA CTACGTTGTT	1920
GGTGCTAGAA CTTTCAGAAG AGAAAAGAGA GCTGAAAGAT TGAATTCTAG AGTTAAGGCT	1980
TTGTTCTCTG TTTTGAAC TAAGAAAGAGCT AGAAGACCAG GTTTGTTGGG TGCTTCTGTT	2040
TTGGGTTTGG ACGACATTCA CAGAGCTTGG AGAACTTTCG TTTTGAGAGT TAGAGCTCAA	2100
GACCCACCAC CAGAATTGTA CTTGTTAAG GTTGACGTTA CTGGTGCTTA CGACACTATT	2160
CCACAAGACA GATTGACTGA AGTTATTGCT TCTATTATTA AGCCACAAAA CACTTACTGT	2220
GTTAGAAGAT ACGCTGTTGT TCAAAAGGCT GCTCACGGTC ACGTTAGAAA GGCTTTCAAG	2280
TCTCACGTTT CTACTTTGAC TGAATTGCAA CCATACATGA GACAATTCGT TGCTCACTTG	2340

CAAGAACTT CTCCATTGAG AGACGCTGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCTTCTTCTG GTTTGTTCGA CGTTTTCTTG AGATTCATGT GTCACCACGC TGTTAGAATT	2460
AGAGGTAAGT CTTACGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTTT GTCTACTTTG	2520
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GGTTTGTGTT TGAGATTGGT TGACGACTTC TTGTTGGTTA CTCCACACTT GACTCACGCT	2640
AAGACTTTCT TGAGAACTTT GGTTAGAGGT GTTCCAGAAT ACGGTTGTGT TGTTAACTTG	2700
AGAAAGACTG TTGTAACTT CCCAGTTGAA GACGAAGCTT TGGGTGGTAC TGCTTTCGTT	2760
CAAATGCCAG CTCACGGTTT GTTCCCATGG TGTGGTTTGT TGTGACAC TAGAACTTTG	2820
GAAGTTCAAT CTGACTACTC TTCTTACGCT AGAACTTCTA TTAGAGCTTC TTTGACTTTC	2880
AACAGAGGTT TCAAGGCTGG TAGAAACATG AGAAGAAAGT TGTTCGGTGT TTTGAGATTG	2940
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TCTTTGTGTT ACTCTATTTT GAAGGCTAAG AACGCTGGTA TGTCTTTGGG TGCTAAGGGT	3180
GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCACCAAGC TTTCTTGTTG	3240
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CCAGCTTTGC CATCTGACTT CAAGACTATT TTGGAC	3396

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "generic" hTERT protein encoding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ATGCCACGTG CCCCACGTTG TCGTGCCGTT CGTTCTTTGT TGCGTTCTCA CTACCGTGAA	60
GTTTTGCCAT TGGCCACCTT CGTTCGTCGT TTGGGTCCAC AAGGTTGGCG TTTGGTTCAA	120
CGTGGTGATC CAGCCGCCTT CCGTGCCTTG GTTGCCCAAT GTTTGGTTTG TGTTCCATGG	180

GATGCCCCGTC	CACCACCAGC	CGCCCCATCT	TTCCGTCAAG	TTTCTTGTTT	GAAAGAATTG	240
GTTGCCCCGTG	TTTTGCAACG	TTTGTGTGAA	CGTGGTGCCA	AAAACGTTTT	GGCCTTCGGT	300
TTCGCCTTGT	TGGATGGTGC	CCGTGGTGGT	CCACCAGAAG	CCTTCACCAC	CTCTGTTCGT	360
TCTTACTTGC	CAAACACCGT	TACCGATGCC	TTGCGTGGTT	CTGGTGCCCTG	GGGTTTGTTG	420
TTGCGTCGTG	TTGGTGATGA	TGTTTTGGTT	CACTTGTTGG	CCCGTTGTGC	CTTGTTTCGTT	480
TTGGTTGCCC	CATCTTGTGC	CTACCAAGTT	TGTGGTCCAC	CATTGTACCA	ATTGGGTGCC	540
GCCACCCAAG	CCCGTCCACC	ACCACACGCC	TCTGGTCCAC	GTCGTCGTTT	GGGTTGTGAA	600
CGTGCCCTGGA	ACCACTCTGT	TCGTGAAGCC	GGTGTTCCAT	TGGGTTTGCC	AGCCCCAGGT	660
GCCCGTCGTC	GTGGTGGTTC	TGCCTCTCGT	TCTTTGCCAT	TGCCAAAACG	TCCACGTCGT	720
GGTGCCGCCC	CAGAACCAGA	ACGTACCCCA	GTTGGTCAAG	GTTCTTGGGC	CCACCCAGGT	780
CGTACCCGTG	GTCCATCTGA	TCGTGGTTTC	TGTGTTGTTT	CTCCAGCCCG	TCCAGCCGAA	840
GAAGCCACCT	CTTTGGAAGG	TGCCTTGTCT	GGTACCCGTC	ACTCTACCC	ATCTGTTGGT	900
CGTCAACACC	ACGCCGGTCC	ACCATCTACC	TCTCGTCCAC	CACGTCCATG	GGATACCCCA	960
TGTCCACCAG	TTTACGCCGA	AACCAAACAC	TTCTTGTA	CTTCTGGTGA	TAAAGAACAA	1020
TTGCGTCCAT	CTTCTTGTT	GTCTTCTTTG	CGTCCATCTT	TGACCGGTGC	CCGTCGTTTG	1080
GTTGAAACCA	TTTTCTTGGG	TTCTCGTCCA	TGGATGCCAG	GTACCCACG	TCGTTTGCCA	1140
CGTTTGCCAC	AACGTTACTG	GCAAATGCGT	CCATTGTTCT	TGGAATTGTT	GGGTAACCAC	1200
GCCCAATGTC	CATACGGTGT	TTTGTTGAAA	ACCCACTGTC	CATTGCGTGC	CGCCGTTACC	1260
CCAGCCGCCG	GTGTTTGTGC	CCGTGAAAAA	CCACAAGGTT	CTGTTGCCGC	CCCAGAAGAA	1320
GAAGATACCG	ATCCACGTCG	TTTGTTTCAA	TTGTTGCGTC	AACACTCTTC	TCCATGGCAA	1380
GTTTACGGTT	TCGTTCTGTC	CTGTTTGCCT	CGTTTGGTTC	CACCAGGTTT	GTGGGGTTCT	1440
CGTCACAACG	AACGTCGTTT	CTTGCGTAAC	ACCAAAAAAT	TCATTTCTTT	GGGTAAACAC	1500
GCCAAATTGT	CTTTGCAAGA	ATTGACCTGG	AAAATGTCTG	TTCGTGATTG	TGCCTGGTTG	1560
CGTCGTTCTC	CAGGTGTTGG	TTGTGTTCCA	GCCGCCGAAC	ACCGTTTGCG	TGAAGAAATT	1620
TTGGCCAAAT	TCTTGCACTG	GTTGATGTCT	GTTTACGTTG	TTGAATTGTT	GCGTTCTTTC	1680
TTCTACGTTA	CCGAAACCAC	CTTCCAAAAA	AACCGTTTGT	TCTTCTACCG	TAAATCTGTT	1740
TGGTCTAAAT	TGCAATCTAT	TGGTATTCGT	CAACACTTGA	AACGTGTTCA	ATTGCGTGAA	1800
TTGTCTGAAG	CCGAAGTTCG	TCAACACCGT	GAAGCCCGTC	CAGCCTTGTT	GACCTCTCGT	1860
TTGCGTTTCA	TTCCAAAACC	AGATGGTTTG	CGTCCAATTG	TTAACATGGA	TTACGTTGTT	1920
GGTGCCCGTA	CCTTCCGTCG	TGAAAAACGT	GCCGAACGTT	TGACCTCTCG	TGTAAAGCC	1980
TTGTTCTCTG	TTTTGAACTA	CGAACGTGCC	CGTCGTCCAG	GTTTGTTGGG	TGCCTCTGTT	2040

TTGGGTTTGG ATGATATTCA CCGTGCCTGG CGTACCTTCG TTTTGCGTGT TCGTGCCCAA	2100
GATCCACCAC CAGAATTGTA CTTCGTTAAA GTTGATGTTA CCGGTGCCTA CGATACCATT	2160
CCACAAGATC GTTTGACCGA AGTTATTGCC TCTATTATTA AACCACAAAA CACCTACTGT	2220
GTTTCGTCGTT ACGCCGTTGT TCAAAAAGCC GCCCACGGTC ACGTTCGTAA AGCCTTCAAA	2280
TCTCACGTTT CTACCTTGAC CGATTTGCAA CCATACATGC GTCAATTCGT TGCCCCACTTG	2340
CAAGAAACCT CTCCATTGCG TGATGCCGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCCTCTTCTG GTTTGTTCTGA TGTTTTCTTG CGTTTCATGT GTCACCACGC CGTTCGTATT	2460
CGTGGTAAAT CTTACGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTTT GTCTACCTTG	2520
TTGTGTTCTT TGTGTTACGG TGATATGGAA AACAAATTGT TCGCCGGTAT TCGTCGTGAT	2580
GGTTTGTTGT TGC GTTTGGT TGATGATTTT TGTGTTGTTA CCCCACACTT GACCCACGCC	2640
AAAACCTTCT TGC GTTACCTT GGTTTCGTGGT GTTCCAGAAT ACGGTTGTGT TGTTAACTTG	2700
CGTAAAACCG TTGTTAACTT CCCAGTTGAA GATGAAGCCT TGGGTGGTAC CGCCTTCGTT	2760
CAAAATGCCAG CCCACGGTTT GTTCCCATGG TGTGGTTTGT TGTTGGATAC CCGTACCTTG	2820
GAAGTTCAAT CTGATTACTC TTCTTACGCC CGTACCTCTA TTCGTGCCTC TTTGACCTTC	2880
AACCGTGGTT TCAAAGCCGG TCGTAACATG CGTCGTAAAT TGTTCCGGTGT TTTGCGTTTG	2940
AAATGTCACT CTTTGTTCTT GGATTTGCAA GTTAACTCTT TGCAAACCGT TTGTACCAAC	3000
ATTTACAAAA TTTTGTTGTT GCAAGCCTAC CGTTTCCACG CCTGTGTTTT GCAATTGCCA	3060
TTCCACCAAC AAGTTTGGA AAACCCAACC TTCTTCTTGC GTGTTATTTT TGATACCGCC	3120
TCTTTGTGTT ACTCTATTTT GAAAGCCAAA AACGCCGTA TGTCTTTGGG TGCCAAAGGT	3180
GCCGCCGGTC CATTGCCATC TGAAGCCGTT CAATGGTTGT GTCACCAAGC CTTCTTGTTG	3240
AAATTGACCC GTCACCGTGT TACCTACGTT CCATTGTTGG GTTCTTTGCG TACCGCCCAA	3300
ACCCAATTGT CTCGTAAATT GCCAGGTACC ACCTTGACCG CCTTGGAAGC CGCCGCCAAC	3360
CCAGCCTTGC CATCTGATTT CAAAACCATT TTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: /note= "oligonucleotide 1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

```

CCAGCGGCAG AACTTCGCGA TAGTGGGAAC GCAGCAGGGA ACGAACAGCA CGGCAACGCG      60
GAGCACGCGG CATATGGTCG ACTCTAGAGC TCCCGCGTGC                          100

```

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 1T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

```

GCACGCGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CGCGTTGCCG TGCTGTTCGT      60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT                                          90

```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```

GGCACTGAGC AACCAGAGCA CGGAAAGCAG CCGGGTCACC ACGCTGAACC AGACGCCAAC      60
CCTGCGGGCC CAGACGACGA ACGAAGGTAG                                          90

```

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

```
CTGCCGCTGG CTACCTTCGT TCGTCGTCTG GGCCCGCAGG GTTGGCGTCT GGTTCAGCGT      60
GGTGACCCGG CTGCTTTCCG TGCTCTGGTT                                         90
```

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

```
GAACACGAGC AACCAGTTCT TTCAGGCAGG AACCTGACG GAAGGACGGA GCAGCCGGCG      60
GCGGACGAGC GTCCCACGGA ACGCAAACCA                                         90
```

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GCTCAGTGCC TGGTTTGCCT TCCGTGGGAC GCTCGTCCGC CGCCGGCTGC TCCGTCCTTC 60

CGTCAGGTTT CCTGCCTGAA AGAACTGGTT 90

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

ATGCTTCCGG CGGACCACCA CGAGCACCGT CCAGCAGAGC GAAACCGAAA GCCAGAACGT 60

TTTAGCACC ACGTTCGCAC AGACGCTGCA 90

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GCTCGTGTTC TGCAGCGTCT GTGCGAACGT GGTGCTAAAA ACCTTCTGGC TTTCGGTTTC 60

GCTCTGCTGG ACGGTGCTCG TGGTGGTCCG 90

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 5B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```
CAACACGACG CAGCAGCAGA CCCAAGCAC CGGAACCACG CAGAGCGTCG GTAACGGTGT      60
TCGGCAGGTA GGAACGAACG GAGGTGGTGA      90
```

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 5T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

```
CCGGAAGCAT TCACCACCTC CGTTCGTTCC TACCTGCCGA ACACCGTTAC CGACGCTCTG      60
CGTG GTTCCG GTGCTTGGGG TCTGCTGCTG      90
```

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GCGGCGGACC ACAAACCTGG TAAGCGCAGG ACGGAGCAAC CAGAACGAAC AGAGCGCAAC 60

GAGCCAGCAG GTGAACCAGA ACGTCGTCAC 90

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CGTCGTGTTG GTGACGACGT TCTGGTTCAC CTGCTGGCTC GTTGCGCTCT GTTCGTTCTG 60

GTTCGCTCCGT CCTGCGCTTA CCAGGTTTGT 90

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 7B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GGTTCCAAGC ACGTTCGCAA CCCAGACGAC GACGCGGACC GGAAGCGTGC GGCGGCGGAC 60

GAGCCTGGGT AGCAGCACCC AGCTGGTACA 90

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 7T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

```
GGTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC      60
GGTCCGCGTC GTCGTCTGGG TTGCGAACGT                                         90
```

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 8B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```
GCAGCGGCAG GGAACGGGAA GCGGAACCAC CACGACGACG AGCACCCGGA GCCGGCAGAC      60
CCAGCGGAAC ACCAGCTTCA CGAACGGAGT                                         90
```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 8T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GCTTGGAACC ACTCCGTTTCG TGAAGCTGGT GTTCCGCTGG GTCTGCCGGC TCCGGGTGCT 60
 CGTCGTCGTG GTGGTTCCGC TTCCCGTTCC 90

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GACCACGGGT ACGACCCGGG TGAGCCCAGG AACCTGACC AACCGGGGTA CGTTCCGGTT 60
 CCGSAGCAGC ACCACGACGC GGACGTTTCG 90

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CTGCCGCTGC CGAAACGTCC GCGTCGTGGT GCTGCTCCGG AACCGGAACG TACCCCGGTT 60
 GGTCAAGGTT CCTGGGCTCA CCCGGGTCGT 90

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 10B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

```
AGTGACGGGT GCCGGACAGA GCACCTTCCA GGGAGGTAGC TTCTTCAGCC GGACGAGCCG      60
GGGAAACAAC GCAGAAACCA CGGTCGGGACG                                     90
```

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 10T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

```
ACCCGTGGTC CGTCCGACCG TGGTTTCTGC GTTGTTTCCC CGGCTCGTCC GGCTGAAGAA      60
GCTACCTCCC TGGAAGGTGC TCTGTCCGGC                                     90
```

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

AAACCGGCGG GCACGGGGTG TCCCACGGAC GCGGCGGACG GGAGGTGGAC GGCGGACCAG 60

CGTGGTGCTG ACGACCAACG GACGGGTGGG 90

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

ACCGGTCACT CCCACCCGTC CGTTGGTCGT CAGCACCACG CTGGTCCGCC GTCCACCTCC 60

CGTCCGCCGC GTCCGTGGGA CACCCCGTGC 90

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 12B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

TCAGGGACGG ACGCAGGGAG GACAGCAGGA AGGACGGACG CAGCTGTTCT TTGTCACCGG 60

AGGAGTACAG GAAGTGTGTTG GTTTCAGCGT 90

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 12T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

```
CCGCCGTTTT ACGCTGAAAC CAAACACTTC CTGTACTCCT CCGGTGACAA AGAACAGCTG      60
CGTCCGTCCT TCCTGCTGTC CTCCTGCGT                                     90
```

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 13B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

```
GCTGCGGCAG ACGCGGCAGA CGACGCGGGG TGCCCGGCAT CCACGGACGG GAACCCAGGA      60
AGATAGTTTC AACCAGACGA CGAGCACCGG                                     90
```

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 13T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTC CCGTCCGTGG 60

ATGCCGGGCA CCCC GCGTCG TCTGCCGCGT 90

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GCGGGCAGTG GGTTTT CAGC AGAACACCAT ACGGGCACTG AGCGTGGTTG CCCAGCAGTT 60

CCAGGAACAG CGGACGCATC TGCCAGTAAC 90

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

CTGCCGCAGC GTTACTGGCA GATGCGTCCG CTGTTCTTGG AACTGCTGGG CAACCACGCT 60

CAGTGCCCGT ATGGTGTCT GCTGAAAACC 90

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
GGTCGGTATC TTCTTCTTCC GGAGCAGCAA CGGAACCCTG CGGTTTTTCA CGAGCGCAAA      60
CACCAGCAGC CGGGGTAACA GCAGCACGCA                                         90
```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```
CACTGCCCCG TCGTGCTGC TGTTACCCCG GCTGCTGGTG TTTGCGCTCG TGAAAAACCG      60
CAGGGTTCCG TTGCTGCTCC GGAAGAAGAA                                         90
```

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GCGGAACCAG ACGACGCAGG CATGCACGAA CGAAACCGTA AACCTGCCAC GGGGAGGAGT 60
 GCTGACGCAG CAGCTGAACC AGACGACGCG 90

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GATACCGACC CGCGTCGTCT GGTTCAGCTG CTGCGTCAGC ACTCCTCCCC GTGGCAGGTT 60
 TACGGTTTCG TTCGTGCATG CCTGCGTCGT 90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 17B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GGGACAGTTT AGCGTGTTTA CCCAGGGAGA TGAATTTTTT GGTGTTACGC AGGAAACGAC 60
 GTTCGTTGTG ACGGGAACCC CACAGACCCG 90

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 17T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

```
CTGGTTCGCG CGGGTCTGTG GGGTTCCCGT CACAACGAAC GTCGTTTCCT GCGTAACACC      60
AAAAAATTCA TCTCCCTGGG TAAACACGCT                                         90
```

(2) INFORMATION FOR SEQ ID NO:677:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 18B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

```
GGTGTTCAGC AGCCGGAACG CAACCAACAC CCGGAGAACG ACGCAGCCAA GCGCAGTCAC      60
GAACGGACAT TTTCCAGGTC AGTTCCTGCA                                         90
```

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 18T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

AAACTGTCCC TGCAGGAAGT GACCTGGAAA ATGTCCGTTT GTGACTGCGC TTGGCTGCGT 60
CGTTCTCCGG GTGTTGGTTG CGTTCCGGCT 90

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CGGTAACGTA GAAGAAGGAA CGCAGCAGTT CAACACGTA TACGGACATC AGCCAGTGCA 60
GGAATTTAGC CAGGATTTCT TCACGCAGAC 90

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GCTGAACACC GTCTGCGTGA AGAAATCCTG GCTAAATTCC TGCAGTGGCT GATGTCCGTA 60
TACGTTGTTG AACTGCTGCG TTCCTTCTTC 90

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 20B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GTTTCAGGTG CTGACGGATA CCGATGGACT GCAGTTTGA CCAAACGGAT TTACGGTAGA	60
AGAACAGACG GTTTTTCTGG AAGGTGGTTT	90

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 20T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

TACGTTACCG AAACCACCTT CCAGAAAAAC CGTCTGTTCT TCTACCGTAA ATCCGTTTGG	60
TCCAAACTGC AGTCCATCGG TATCCGTCAG	90

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: /note= "oligonucleotide 21B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GATGAAACGC AGACGGGAGG TCAGCAGAGC CGGACGAGCT TCACGGTGCT GACGAACTTC 60

AGCTTCGGAC AGTTCACGCA GCTGAACAC 89

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 21T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

CACCTGAAAC GTGTTACAGT GCGTGAAGCTG TCCGAAGCTG AAGTTCGTCA GCACCGTGAA 60

GCTCGTCCGG CTCTGCTGAC CTCCCGTCTG 90

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

TCAGACGCTC AGCACGTTTT TCACGACGGA AGGTACGAGC ACCAACAACG TAGTCCATGT 60

TTACGATCGG ACGCAGACCG TCCGGTTTCG 90

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CGTTTCATCC CGAAACCGGA CGGTCTGCGT CCGATCGTAA ACATGGACTA CGTTGTTGGT	60
GCTCGTACCT TCCGTCGTGA AAAACGTGCT	90

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CGTCCAGACC CAGAACGGAA GCACCCAGCA GACCCGGACG ACGAGCACGT TCGTAGTTCA	60
GAACGGAGAA CAGAGCTTTA ACACGGGAGG	90

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAGCGTCTGA CCTCCCGTGT TAAAGCTCTG TTCTCCGTTC TGAACACGA ACGTGCTCGT 60

CGTCCGGGTC TGCTGGGTGC TTCCGTTCTG 90

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

CGGTAACGTC AACTTTAACG AAGTACAGTT CCGGCGGCGG GTCCTGAGCA CGAACACGCA 60

GAACGAAGGT ACGCCAAGCA CGGTGGATGT 90

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGTCTGGACG ACATCCACCG TGCTTGGCGT ACCTTCGTTC TGCGTGTTTCG TGCTCAGGAC 60

CCGCCGCCGG AACTGTACTT CGTTAAAGTT 90

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 25B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

CGTAACGACG AACGCAGTAG GTGTTCTGCG GTTTGATGAT GGAAGCGATA ACTTCGGTCA	60
GACGGTCCTG CGGGATGGTG TCGTACGCGC	90

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 25T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GACGTTACCG GCGCGTACGA CACCATCCCG CAGGACCGTC TGACCGAAGT TATCGCTTCC	60
ATCATCAAAC CGCAGAACAC CTACTGCGTT	90

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GACGCATGTA CGGCTGCAGG TCGGTCAGGG TGGAAACGTG GGATTTGAAT GCTTTACGAA 60
 CGTGACCGTG AGCAGCTTTC TGAACAACAG 90

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

CGTCGTTACG CTGTTGTTCA GAAAGCTGCT CACGGTCACG TTCGTAAAGC ATTCAAATCC 60
 CACGTTTCCA CCCTGACCGA CCTGCAGCCG 90

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 27B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GACCGGAGGA AGCTTCGTTT AGGGAGGAGG ACTGTTTCGAT AACAAACAGCG TCACGCAGCG 60
 GGGAGGTTTC CTGCAGGTGA GCAACGAACT 90

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 27T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

TACATGCGTC AGTTCGTTGC TCACCTGCAG GAAACCTCCC CGCTGCGTGA CGCTGTTGTT	60
ATCGAACAGT CCTCCTCCCT GAACGAAGCT	90

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 28B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

AACCCTGCGG GATACCCTGG CACTGAACGT AGGATTTACC ACGGATACGA ACAGCGTGGT	60
GGCACATGAA ACGCAGGAAA ACGTCGAACA	90

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 28T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TCCTCCGGTC TGTTTCGACGT TTTCTGCGT TTCATGTGCC ACCACGCTGT TCGTATCCGT	60
GGTAAATCCT ACGTTCAGTG CCAGGGTATC	90

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GCAGCAGCAG ACCGTCACGA CGGATACCAG CGAACAGTTT GTTTTCCATG TCACCGTAGC	60
ACAGGGAGCA CAGCAGGGTG GACAGGATGG	90

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

CCGCAGGGTT CCATCCTGTC CACCCTGCTG TGCTCCCTGT GCTACGGTGA CATGGAAAAC	60
AAACTGTTTCG CTGGTATCCG TCGTGACGGT	90

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

```
CGTATTCCGG AACACCACGA ACCAGGGTAC GCAGGAAGGT TTAGCGTGG GTCAGGTGCC      60
GAGTAACCAG CAGGAAGTCG TCAACCAGAC                                     90
```

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

```
CTGCTGCTGC GTCTGGTTGA CGACTTCCTG CTGGTTACTC CGCACCTGAC CCACGCTAAA      60
ACCTTCCTGC GTACCCTGGT TCGTGGTGTG                                     90
```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAGCCGGCAT CTGAACGAAA GCGGTGCCAC CCAGAGCTTC GTCTTCAACC GGGAAGTTAA 60

CAACGGTTTT ACGCAGGTTT ACAACGCAAC 90

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

CCGGAATACG GTTGCGTTGT AAACCTGCGT AAAACCGTTG TTAATTCCC GGTTGAAGAC 60

GAAGCTCTGG GTGGCACCGC TTTCGTTTCA 90

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGATGGAGGT ACGAGCGTAG GAGGAGTAGT CGGACTGAAC TTCCAGGGTA CGGGTGTCCA 60

GCAGCAGACC GCACCACGGG AACAGACCGT 90

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

ATGCCGGCTC ACGGTCTGTT CCCGTGGTGC GGTCTGCTGC TGGACACCCG TACCCTGGAA	60
GTTCAGTCCG ACTACTCCTC CTACGCTCGT	90

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GGGAGTGGCA TTTCAGACGC AGAACACCGA ACAGTTTACG ACGCATGTTA CGACCAGCTT	60
TGAAACCACG GTTGAAGGTC AGGGAAGCAC	90

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ACCTCCATCC GTGCTTCCCT GACCTTCAAC CGTGGTTTCA AAGCTGGTCG TAACATGCGT 60

CGTAAACTGT TCGGTGTTCT GCGTCTGAAA 90

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

ACGCGTGGAAC ACGGTAAGCC TGCAGCAGCA GGATTTTGTA GATGTTGGTG CAAACGGTCT 60

GCAGGGAGTT TACCTGCAGG TCCAGGAACA 90

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TGCCACTCCC TGTTCTGGA CCTGCAGGTA AACTCCCTGC AGACCGTTTG CACCAACATC 60

TACAAAATCC TGCTGCTGCA GGCTTACCGT 90

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 35B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

AGTAGCACAG GGAAGCGGTG TCGGAGATAA CACGCAGGAA GAAGGTCGGG TTTTCCAAA	60
CCTGCTGGTG GAACGGCAGC TGCAGAACGC	90

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 35T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

TTCCACGCGT GCGTTCTGCA GCTGCCGTTT CACCAGCAGG TTTGGAAAAA CCCGACCTTC	60
TTCCTGCGTG TTATCTCCGA CACCGCTTCC	90

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GGCACAGCCA CTGAACAGCT TCGGACGGCA GCGGACCAGC AGCACCTTTA GCACCCAGGG 60

ACATACCAGC GTTTTtagCT TTCAGGATGG 90

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

CTGTGCTACT CCATCCTGAA AGCTAAAAAC GCTGGTATGT CCCTGGGTGC TAAAGGTGCT 60

GCTGGTCCGC TGCCGTCCGA AGCTGTTTCA 90

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: /note= "oligonucleotide 37B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

ACAGCTGGGT CTGAGCGGTA CGCAGGGAAC CCAGCAGCGG AACGTAGGTA ACACGGTGAC 60

GGGTCAGTTT CAGCAGGAAA GCCTGGT 87

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: /note= "oligonucleotide 37T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG	60
CTGCTGGGTT CCCTGCGTAC CGCTCAG	87

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "oligonucleotide 38B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

ACGGCAGAGC CGGGTTAGCA GCAGCTTCCA GAGCGGTCAG GGTGGTACCC GGCAGTTTAC	60
GGG	63

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: /note= "oligonucleotide 38T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC 60
 CCGG 64

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "oligonucleotide 39B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GCGTGCCTCG AGGAATTCGG ATCCATTAGT CCAGGATGGT TTTGAAGTCG 50

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide 39T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

CTCTGCCGTC CGACTTCAAA ACCATCCTGG ACTAATGGAT CCGAATTCCT CGAGGCACGC 60

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3451
- (D) OTHER INFORMATION: /note= "hTRT sequence employing codon distribution preferentially used by highly expressed genes in E. coli containing SacI and XhoI sites"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

```

GCACGCGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CGCGTTGCCG TGCTGTTCGT      60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT CTGCCGCTGG CTACCTTCGT TCGTCGCTCG      120
GGCCCGCAGG GTTGCGTCT GTTCAGCGT GGTGACCCGG CTGCTTTCCG TGCTCTGGTT      180
GCTCAGTGCC TGGTTTGCGT TCCGTGGGAC GCTCGTCCGC CGCCGGCTGC TCCGTCCTTC      240
CGTCAGGTTT CCTGCCTGAA AGAACTGGTT GCTCGTGTTC TGCAGCGTCT GTGCGAACGT      300
GGTGCTAAAA ACGTTCTGGC TTTCGGTTTC GCTCTECTGG ACGGTGCTCG TGGTGGTCCG      360
CCGGAAGCAT TCACCACCTC CGTTCGTTCC TACCTGCCGA ACACCGTTAC CGACGCTCTG      420
CGTGGTTCCG GTGCTTGCGG TCTGCTGCTG CGTCGTGTTG GTGACGACGT TCTGGTTTAC      480
CTGCTGGCTC GTTGCGCTCT GTTCGTTCTG GTTGCTCCGT CCTGCGCTTA CCAGGTTTGT      540
GGTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC      600
GGTCCGCGTC GTCGTCTGGG TTGCGAACGT GCTTGAAC ACCCGTTTCG TGAAGCTGGT      660
GTTCCGCTGG GTCTGCCGGC TCCGGGTGCT CGTCGTCTGT GTGGTTCCGC TTCCCGTTCC      720
CTGCCGCTGC CGAAACGTCC GCGTCGTGGT GCTGCTCCGG AACCGBAACG TACCCCGGTT      780
GGTCAGGGTT CCTGGGCTCA CCCGGGTGCT ACCCGTGGTC CGTCCGACCG TGGTTTCTGC      840
GTTGTTTCCC CGGCTCGTCC GGCTGAAGAA GCTACCTCCC TGGAAGGTGC TCTGTCCGGC      900
ACCCGTCACT CCCACCCGTC CGTTGGTCGT CAGCACCACG CTGGTCCGCC GTCCACCTCC      960
CGTCCGCCGC GTCCGTGGGA CACCCCGTGC CCGCCGTTT ACGCTGAAAC CAAACACTTC     1020
CTGTACTCCT CCGGTGACAA AGAACAGCTG CGTCCGTCTT TCCTGCTGTC CTCCCTGCGT     1080
CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTC CCGTCCGTGG     1140
ATGCCGGGCA CCCCAGCTCG TCTGCCGCGT CTGCCGCAGC GTTACTGGCA GATGCGTCCG     1200

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CTGTTCCCTGG AACTGCTGGG CAACCACGCT CAGTGCCCGT ATGGTGTTCCT GCTGAAAACC	1260
CACTGCCCCG TGCCTGCTGC TGTTACCCCG GCTGCTGGTG TTTGCGCTCG TGAAAAACCG	1320
CAGGGTTCCG TTGCTGCTCC GGAAGAAGAA GATACCGACC CGCGTCGTCT GGTTTCAGCTG	1380
CTGCGTCAGC ACTCCTCCCC GTGGCAGGTT TACGGTTTCG TTCGTGCATG CCTGCGTCGT	1440
CTGGTTCCGC CGGGTCTGTG GGGTTCCCGT CACAACGAAC GTCGTTTCCT GCGTAACACC	1500
AAAAAATTCA TCTCCCTGGG TAAACACGCT AACTGTCCC TGCAGGAACT GACCTGGAAA	1560
ATGTCCGTTT GTGACTGCGC TTGGCTGCGT CGTTCTCCGG GTGTTGGTTG CGTTCCGGCT	1620
GCTGAACACC GTCTGCGTGA AGAAATCCTG GCTAAATTCC TGCCTGGCT GATGTCCGTA	1680
TACGTTGTTG AACTGCTGCG TTCCTTCTTC TACGTTACCG AAACCACCTT CCAGAAAAAC	1740
CGTCTGTTCT TCTACCGTAA ATCCGTTTGG TCCAACTGC AGTCCATCGG TATCCGTCAG	1800
CACCTGAAAC GTGTTTCAGCT GCGTGAAGTG TCCGAAGCTG AAGTTCGTCA GCACCGTGAA	1860
GCTCGTCCGG CTCTGCTGAC CTCCCGTCTG CGTTTCATCC CGAAACCGGA CGGTCTGCGT	1920
CCGATCGTAA ACATGGACTA CGTTGTTGGT GCTCGTACCT TCCGTCGTGA AAAACGTGCT	1980
GACCGTCTGA CCTCCCGTGT TAAAGCTCTG TTCTCCGTTT TGAACACGA ACGTGCTCGT	2040
CGTCCGGGTC TGCTGGGTGC TTCCGTTCTG GGTCTGGACG ACATCCACCG TGCTTGGCGT	2100
ACCTTCGTTT TGCCTGTTTC TGCTCAGGAC CCGCCGCCGG AACTGTACTT CGTTAAAGTT	2160
GACGTTACCG GCGCGTACGA CACCATCCCC CAGGACCGTC TGACCGAAGT TATCGCTTCC	2220
ATCATCAAAC CGCAGAACAC CTAATGCGTT CGTCGTTACG CTGTTGTTCA GAAAGCTGCT	2280
CACGGTCACG TTCGTAAAGC ATTCAAATCC CACGTTTCCA CCCTGACCGA CCTGCAGCCG	2340
TACATGCGTC AGTTCGTTGC TCACCTGCAG GAAACCTCCC CGCTGCGTGA CGCTGTTGTT	2400
ATCGAACAGT CCTCCTCCCT GAACGAAGCT TCCTCCGGTC TGTTGACGT TTTCTGCGT	2460
TTTATGTGCC ACCACGCTGT TCGTATCCGT GGTAAATCCT ACGTTTCAGT CCAGGGTATC	2520
CCGCAGGGTT CCATCCTGTC CACCCTGCTG TGCTCCCTGT GCTACGGTGA CATGGAAAAC	2580
AAACTGTTTC CTGGTATCCG TCGTGACGGT CTGCTGCTGC GTCTGGTTGA CGACTTCCTG	2640
CTGTTTACTC CGCACCTGAC CCACGCTAAA ACCTTCCTGC GTACCCTGGT TCGTGGTGTT	2700
CCGGAATACG GTTGCCTTGT AAACCTGCGT AAAACCGTTG TTAACCTCCC GGTTGAAGAC	2760
GAGCTCTGG GTGGCACCGC TTTGCTTCAG ATGCCGGCTC ACGGTCTGTT CCCGTGGTGC	2820
GGTCTGCTGC TGGACACCCG TACCCTGGAA GTTCAGTCCG ACTACTCCTC CTACGCTCGT	2880
ACCTCCATCC GTGCTTCCCT GACCTTCAAC CGTGGTTTCA AAGCTGGTCG TAACATGCGT	2940
CGTAAACTGT TCGGTGTTCT GCGTCTGAAA TGCCACTCCC TGTTCTGGA CCTGCAGGTA	3000
AACTCCCTGC AGACCGTTTG CACCAACATC TACAAAATCC TGCTGCTGCA GGCTTACCGT	3060

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TTCCACGCGT GCGTTCTGCA GCTGCCGTTT CACCAGCAGG TTTGGAAAAA CCCGACCTTC 3120
TTCCTGCGTG TTATCTCCGA CACCGCTTCC CTGTGCTACT CCATCCTGAA AGCTAAAAAC 3180
GCTGGTATGT CCCTGGGTGC TAAAGGTGCT GCTGGTCCGC TGCCGTCCGA AGCTGTTTAC 3240
TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG 3300
CTGCTGGGTT CCCTGCGTAC CGCTCAGACC CAGCTGTCCC GTAAACTGCC GGGTACCACC 3360
CTGACCGCTC TGGAAGCTGC TGCTAACCCG GCTCTGCCGT CCGACTTCAA AACCATCCTG 3420
GACTAATGGA TCCGAATTCC TCGAGGCACG C 3451

```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
31-60 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

```
GGCATCGCGG GGGTGGCCGG GGCCAGGGCT 30
```

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
496-525 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

```
GCGCAGCGTG CCAGCAGGTG AACCAGCACG 30
```

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
631-660 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GCCCGTTTCGC ATCCCAGACG CCTTCGGGGT

30

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
646-675 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

ACGCTATGGT TCCAGGCCCG TTCGCATCCC

30

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: /note= "sequence present in pGRN176 but not pGRN175"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

GTGGCGGAGG GACTGGGGAC CCGGGCACCG GTCCTGCCCC TTCACCTTCC AGCTCCGCCT      60
CGTCCGCGCG GAACCCCGCC CCGTCCCGAA CCCTTCCCGG GTCCCCGGCC CAGCCCCTTC      120
CGGG                                              124

```

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1-300 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at position 630 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 649-663 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 674-688 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 701-706 may be present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 771..790

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 771-790 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 887..937

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 887-937 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 965..994

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 965-994 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1018..1027

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1018-1027 may
be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35					40					45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			50					55					60		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65						70					75				80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85							90					95

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100							105				110	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			115							120				125	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			130							135				140	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145						150					155				160

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
165								170				175			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
180								185				190			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
195								200				205			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
210								215				220			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
225								230				235			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
240								245				250			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
255								260				265			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
270								275				280			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
285								290				295			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
300								305				310			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
315								320				325			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
330								335				340			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
345								350				355			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
360								365				370			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
375								380				385			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
390								395				400			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
405								410				415			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
420								425				430			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
435								440				445			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
450								455				460			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
465								470				475			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
480								485				490			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	485	490	495
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	500	505	510
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	515	520	525
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	530	535	540
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	545	550	555
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	565	570	575
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	580	585	590
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	595	600	605
Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr	Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	610	615	620
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	625	630	635
Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	645	650	655
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	660	665	670
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	675	680	685
Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	690	695	700
Xaa	Xaa	Arg	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	705	710	715
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	725	730	735
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	740	745	750
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	755	760	765
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	770	775	780
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Asp	Xaa	785	790	795
																		800

B'